

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME : GENSET SA
- (B) STREET : 24, RUE ROYALE
- (C) CITY: PARIS
- (E) COUNTRY : FRANCE
- (F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES

(iii) NUMBER OF SEQUENCES: 573

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy Disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: Win95
- (D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(ix) FEATURE:

- (A) NAME/KEY: Cap
- (B) LOCATION: 1
- (D) OTHER INFORMATION: m7Gppp added to 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCAUCCUAC UCCCAUCCAA UCCACCCUA ACUCCUCCCA UCUCAC

47

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GCAUCCUACU CCAUCCAAU UCCACCCUAA CUCCUCCCAU CUCAC

46

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATCAAGAATT CGCAGGAGAC CATTG

25

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAATGGTCTC GTGCGAATTC TTGAT

25

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CCGACAAGAC CAACGTCAAG GCCGC

25

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

TCACCAGCAG GCAGTGGCTT AGGAG

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AGTGATTCCT GCTACTTTGG ATGGC

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCTTGGTCTT GTTCTGGAGT TTAGA

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCCAGAATGG GAGACAAGCC AATTT

25

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGGGAGGAGG AAACAGCGTG AGTCC

25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGGGAAAGG AAAAGACTCA TATCA

25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AGCAGCAACA ATCAGGACAG CACAG

25

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCAAGAATT CGCAGGAGAC CATTA

25

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ATCGTTGAGA CTCGTACCAG CAGAGTCACG AGAGAGACTA CACGGTACTG GTTTTTTTTTT

60

TTTTTVN

67

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CCAGCAGAGT CACGAGAGAG ACTACACGG

29

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CACGAGAGAG ACTACACGGT ACTGG

25

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 526 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(261..376)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 166..281
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(380..486)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 54..160
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(110..145)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 403..438
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(196..229)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 31..348
 id N70479
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 90..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.2
 seq LLLITAILAVVG/FP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AATATRARAC AGCTACAATA TTCCAGGGCC ARTCACTTGC CATTCTCAT AACAGCGTCA 60
GAGAGAAAGA ACTGACTGAR ACGTTTGAG ATG AAG AAA GTT CTC CTC CTG ATC 113

Met Lys Lys Val Leu Leu Leu Ile
-15 -10

ACA GCC ATC TTG GCA GTG GCT GTW GGT TTC CCA GTC TCT CAA GAC CAG 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5

GAA CGA GAA AAA AGA AGT ATC AGT GAC AGC GAT GAA TTA GCT TCA GGR 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20

WTT TTT GTG TTC CCT TAC CCA TAT CCA TTT CGC CCA CTT CCA CCA ATT 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35

CCA TTT CCA AGA TTT CCA TGG TTT AGA CGT AAN TTT CCT ATT CCA ATA 305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40 45 50 55

CCT GAA TCT GCC CCT ACA ACT CCC CTT CCT AGC GAA AAG TAAACAARAA 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65

GGAAAAGTCA CRATAACCT GGTACCTGA AATTGAAATT GAGCCACTTC CTTGAARAAT 414

CAAAATTCCT GTTAATAAAA RAAAAACAAA TGTAATTGAA ATAGCACACA GCATTCTCTA 474

GTCAATATCT TTAGTGATCT TCTTTAATAA ACATGAAAGC AAAAAAAAAA AA 526

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..17
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.2
seq LLLITAILAVAVG/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 822 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 260..464
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 96
region 153..357
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 118..184
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 98..164
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 56..113
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 35..92
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 454..485
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 100
region 348..379
id H57434
est
- (ix) FEATURE:
 - (A) NAME/KEY: other
 - (B) LOCATION: 118..545
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 1..428
id N27248
est
- (ix) FEATURE:
 - (A) NAME/KEY: other

(B) LOCATION: 65..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 1.
region 41..345
id H94779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 6..344
id H09880
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 408..458
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 355..405
id H09880
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 56..395
id H29351
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 393..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 391..430
id H29351
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 346..408
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

| | |
|---|-----|
| ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CTAGTCGGTC TGGTAAGTGC | 60 |
| CTGATGCCSA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGSCAAAGCG GASGNAGATC | 120 |
| CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTG | 180 |
| GTTTGTGAA GCAGITACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA | 240 |

| | |
|---|-----|
| CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG | 300 |
| AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT | 357 |
| Met Trp Trp Phe -20 | |
| CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT | 405 |
| Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser -15 -10 -5 | |
| GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA | 453 |
| Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile 1 5 10 15 | |
| GAC CCG GCT TTA CCT TAT ATC AGT GAC ACT GGT ACA GTA GCT CCA RAA | 501 |
| Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa 20 25 30 | |
| AAA TGC TTA TTT GGG GCA ATG CTA AAT ATT GCG GCA GTT TTA TGT CAA | 549 |
| Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln 35 40 45 | |
| AAA TAGAAATCAG GAARATAATT CAACTTAAAG AAKTTCATTT CATGACCAAA | 602 |
| Lys | |
| CTCTTCARAA ACATGTCTTT ACAAGCATAT CTCTTGATT GCTTTCTACA CTGTTGAATT | 662 |
| GTCTGGCAAT ATTTCTGCAG TGGAAAATTT GATTTARMTA GTTCTTGACT GATAAATATG | 722 |
| GTAAGGTGGG CTTTTCCCC TGTGTAATTG GCTACTATGT CTTACTGAGC CAAGTTGTAW | 782 |
| TTTGAAATAA AATGATATGA GAGTGACACA AAAAAAAAAA | 822 |

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..21
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
1 5 10 15

Ile Trp Thr Ser Ala
20

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(103..398)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..296
id AA442893
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 185..295
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LSYASSALSPCLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ATCACCTTCT TCTCCATCCT TSTCTGGGCC AGTCCCCARC CCAGTCCCTC TCCTGACCTG      60
CCCAGCCCCAA GTCAGCCTTC AGCACGCGCT TTTCTGCACA CAGATATTCC AGGCCTACCT      120
GGCATTCCAG GACCTCCGMA ATGATGCTCC AGTCCCTTAC AAGCGCTTCC TGGATGAGGG      180
TGGC ATG GTG CTG ACC ACC CTC CCC TTG CCC TCT GCC AAC AGC CCT GTG      229
    Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val
        -35                -30                -25

AAC ATG CCC ACC ACT GGC CCC AAC AGC CTG AGT TAT GCT AGC TCT GCC      277
Asn Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala
    -20                -15                -10

CTG TCC CCC TGT CTG ACC GCT CCA AAK TCC CCC CGG CTT GGT ATG ATG      325
Leu Ser Pro Cys Leu Thr Ala Pro Xaa Ser Pro Ala Leu Ala Met Met
    -5                1                5                10

CCT GAC AAC TAAATATCCT TATCCAAATC AATAAARWRA RAATCCTCCC TCCARAAGGG      384
Pro Asp Asn

TTTCTAAAAA CAAAAA AAAA A

```

405

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..37
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LSYASSALSPCLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Val Leu Thr Thr Leu Pro Leu Pro Ser Ala Asn Ser Pro Val Asn
1 5 10 15
Met Pro Thr Thr Gly Pro Asn Ser Leu Ser Tyr Ala Ser Ser Ala Leu
20 25 30
Ser Pro Cys Leu Thr
35

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..183
id AA397994
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 328..485
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 179..336
 id AA397994
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(182..496)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 14..328
 id AA399680
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 196..240
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq ILSTVRLTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

AAAAAATTGG TCCCAGTTTT CACCCTGCCG CAGGGCTGGC TGGGGAGGGC AGCGGTTTAG      60
ATTAGCCGTG GCCTAGGCCG TTTAACGGGG TGACACGAGC NTGCAGGGCC GAGTCCAAGG      120
CCCGGAGATA GGACCAACCG TCAGGAATGC GAGGAATGTT TTTCTTCGGA CTCTATCGAG      180
GCACACAGAC AGACC ATG GGG ATT CTG TCT ACA GTG ACA GCC TTA ACA TTT      231
      Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe
      -15                      -10                      -5

GCC ARA GCC CTG GAC GGC TGC AGA AAT GGC ATT GCC CAC CCT GCA AGT      279
Ala Xaa Ala Leu Asp Gly Cys Arg Asn Gly Ile Ala His Pro Ala Ser
      1                      5                      10

GAG AAG CAC AGA CTC GAG AAA TGT AGG GAA CTC GAG ASC ASC CAC TCG      327
Glu Lys His Arg Leu Glu Lys Cys Arg Glu Leu Glu Xaa Xaa His Ser
      15                      20                      25

GCC CCA GGA TCA ACC CAS CAC CGA AGA AAA ACA ACC AGA AGA AAT TAT      375
Ala Pro Gly Ser Thr Xaa His Arg Arg Lys Thr Thr Arg Arg Asn Tyr
      30                      35                      40                      45

TCT TCA GCC TGAATGAAK CCGGGATCAA ATGGTTGCTG ATCARAGCCC ATATTTAAAT      434
Ser Ser Ala

TGGAAAAGTC AAATTGASCA TTATTAAATA AAGCTTGTTT AATATGTCTC AAACAAAAAA      494
AA                                                                 496
  
```

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..15
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq ILSTVTALTFAXA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```
Met Gly Ile Leu Ser Thr Val Thr Ala Leu Thr Phe Ala Xaa Ala
 1             5             10             15
```

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 623 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 49..96
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.1
seq LVLTLCCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```
AAAGATCCCT GCAGCCCGGC AGGAGAGAAG GCTGAGCCTT CTGGCGTC ATG GAG AGG      57
                                         Met Glu Arg
                                         -15

CTC GTC CTA ACC CTG TGC ACC CTC CCG CTG GCT GTG GCG TCT GCT GGC      105
Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
-10             -5             1

TGC GCC ACG ACG CCA GCT CGC AAC CTG AGC TGC TAC CAG TGC TTC AAG      153
Cys Ala Thr Thr Pro Ala Arg Asn Leu Ser Cys Tyr Gln Cys Phe Lys
 5             10             15

GTC ACC AGC TGG ACG GAG TGC CCG CCC ACC TGG TGC AGC CCG CTG GAC      201
```

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Ser | Trp | Thr | Glu | Cys | Pro | Pro | Thr | Trp | Cys | Ser | Pro | Leu | Asp | |
| 20 | | | | | 25 | | | | | 30 | | | | | 35 | |
| CAA | GTC | TGC | ATC | TCC | AAC | GAG | GTG | GTC | GTC | TCT | TFT | AAA | TGG | AGT | GTA | 249 |
| Gln | Val | Cys | Ile | Ser | Asn | Glu | Val | Val | Val | Ser | Phe | Lys | Trp | Ser | Val | |
| | | | 40 | | | | | 45 | | | | | 50 | | | |
| CGC | GTC | CTG | CTC | AGC | AAA | CGC | TGT | GCT | CCC | AGA | TGT | CCC | AAC | GAC | AAC | 297 |
| Arg | Val | Leu | Leu | Ser | Lys | Arg | Cys | Ala | Pro | Arg | Cys | Pro | Asn | Asp | Asn | |
| | | 55 | | | | | 60 | | | | | 65 | | | | |
| ATG | AAK | TTC | GAA | TGG | TCG | CCG | GCC | CCC | ATG | GTG | CAA | GGC | GTG | ATC | ACC | 345 |
| Met | Xaa | Phe | Glu | Trp | Ser | Pro | Ala | Pro | Met | Val | Gln | Gly | Val | Ile | Thr | |
| | 70 | | | | | 75 | | | | | 80 | | | | | |
| AGG | CGC | TGC | TGT | TCC | TGG | GCT | CTC | TGC | AAC | AGG | GCA | CTG | ACC | CCA | CAG | 393 |
| Arg | Arg | Cys | Cys | Ser | Trp | Ala | Leu | Cys | Asn | Arg | Ala | Leu | Thr | Pro | Gln | |
| | 85 | | | | | 90 | | | | 95 | | | | | | |
| GAG | GGG | CGC | TGG | GCC | CTG | CRA | GGG | GGG | CTC | CTG | CTC | CAG | GAC | CCT | TCG | 441 |
| Glu | Gly | Arg | Trp | Ala | Leu | Xaa | Gly | Gly | Leu | Leu | Gln | Asp | Pro | Ser | | |
| 100 | | | | 105 | | | | 110 | | | | | | 115 | | |
| AGG | GGC | ARA | AAA | ACC | TGG | GTG | CGG | CCA | CAG | CTG | GGG | CTC | CCA | CTC | TGC | 489 |
| Arg | Gly | Xaa | Lys | Thr | Trp | Val | Arg | Pro | Gln | Leu | Gly | Leu | Pro | Leu | Cys | |
| | | | 120 | | | | 125 | | | | | 130 | | | | |
| CTT | CCC | AWT | TCC | AAC | CCC | CTC | TGC | CCA | RGG | GAA | ACC | CAG | GAA | GGA | | 534 |
| Leu | Pro | Xaa | Ser | Asn | Pro | Leu | Cys | Pro | Xaa | Glu | Thr | Gln | Glu | Gly | | |
| | | 135 | | | | 140 | | | | | 145 | | | | | |
| TAACACTGTG | GGTGCCCCCA | CCTGTGCATT | GGGACCACRA | CTTCACCCTC | TTGGARACAA | | | | | | | | | | | 594 |
| TAAACTCTCA | TGCCCCCAAA | AAAAAAAAAA | | | | | | | | | | | | | | 623 |

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..16
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1
seq LVLTLCTLPLAVA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Leu | Val | Leu | Thr | Leu | Cys | Thr | Leu | Pro | Leu | Ala | Val | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 32..73
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT CTG      55
                               Met Leu Trp Leu Leu Phe Phe Leu
                               -10

GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT GCT      103
Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn Ala
-5                               1                               5                               10

TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA TAT      151
Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala Tyr
15                               20                               25

GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT TTC      199
Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala Phe
30                               35                               40

TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT GTC      247
Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His Val
45                               50                               55

CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT ACA      295
Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val Thr
60                               65                               70

GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA GCC      343
Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser Ala
75                               80                               85                               90

ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GCC TTC TTT CTA AAT GAC      391
Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn Asp
95                               100                               105

CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA CCC ATG      439

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| | |
|---|-----|
| Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro Met | |
| 110 115 120 | |
| GAC CCA TCT GTG CCC ATC TGG ATT ATT ATA TTT GGT GTG ATA TTT TGC | 487 |
| Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe Cys | |
| 125 130 135 | |
| ATC ATC ATA GTT GCA ATT GCA CTA CTG ATT TTA TCA GGG ATC TGG CAA | 535 |
| Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp Gln | |
| 140 145 150 | |
| CGT ADA ARA AAG AAC AAA GAA CCA TCT GAA GTG GAT GAC GCT GAA RAT | 583 |
| Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu Xaa | |
| 155 160 165 170 | |
| AAK TGT GAA AAC ATG ATC ACA ATT GAA AAT GGC ATC CCC TCT GAT CCC | 631 |
| Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp Pro | |
| 175 180 185 | |
| CTG GAC ATG AAG GGA GGG CAT ATT AAT GAT GCC TTC ATG ACA GAG GAT | 679 |
| Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu Asp | |
| 190 195 200 | |
| GAG AGG CTC ACC CCT CTC TGAAGGGCTG TTGTTCTGCT TCCTCAARAA | 727 |
| Glu Arg Leu Thr Pro Leu | |
| 205 | |
| ATTAAACATT TGTTTCTGTG TGACTGCTGA GCATCCTGAA ATACCAAGAG CAGATCATAT | 787 |
| WTTTGTGTTT ACCATTCTTC TTTTGTAATA AATTTTGAAT GTGCTTGAAA AAAAAAAAAA | 847 |
| C | 848 |

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..14
- (C) IDENTIFICATION METHOD: Von Helme matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFHLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

| |
|---|
| Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala |
| 1 5 10 |

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGAAGATGG AGATAGTATT GCCTG

25

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTGCCATGTA CATGATAGAG AGATTG

26

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..517

(ix) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 518

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 17..25
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.933
sequence TGTCACTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(18..27)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MYOD_Q6
score 0.961
sequence CCCAACTGAC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(75..85)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.960
sequence AATAGAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 94..104
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name S8_01
score 0.966
sequence AACTAAATTAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(129..139)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name DELTAEF1_01
score 0.960
sequence GCACACCTCAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(155..165)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C
score 0.964
sequence AGATAAATCCA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 170..178
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_Q1
score 0.958
sequence CTCAGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 176..189
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA1_02
score 0.959
sequence TTGTAGATAGGACA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 180..190
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA_C

score 0.953
sequence AGATAGGACAT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 284..299
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name TAL1ALPHAE47_01
score 0.973
sequence CATAACAGATGGTAAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 284..299
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name TAL1BETAE47_01
score 0.983
sequence CATAACAGATGGTAAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 284..299
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name TAL1BETAITF2_01
score 0.978
sequence CATAACAGATGGTAAG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(287..296)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MYOD_Q6
score 0.954
sequence ACCATCTGTT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(302..314)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name GATA1_04
score 0.953
sequence TCAAGATAAAGTA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 393..405
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK1_01
score 0.963
sequence AGTTGGGAATTCC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 393..404
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK2_01
score 0.935
sequence AGTTGGGAATTC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GTACCAGGGA CTGTGACCAT TGC

23

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: SINGLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGTGACCAT TGCTCCCAAG AGAG

24

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 861 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..806

(ix) FEATURE:

- (A) NAME/KEY: transcription start site
- (B) LOCATION: 807

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(60..70)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name NFY_Q6
score 0.956
sequence GGACCAATCAT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 70..77
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.962
sequence CCTGGGGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 124..132
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name CMYB_01
score 0.994
sequence TCACCGTTG

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(126..134)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name VMYB_02
score 0.985
sequence TCCAACGGT

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 135..143
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.968
sequence TTCCTGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(135..143)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name STAT_01
score 0.951
sequence TTCCAGGAA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: complement(252..259)
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name MZF1_01
score 0.956
sequence TTGGGGGA

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 357..368
- (C) IDENTIFICATION METHOD: matinspector prediction
- (D) OTHER INFORMATION: name IK2_01
score 0.965
sequence GAATGGGATTTC

(ix) FEATURE:

- (A) NAME/KEY: TF binding-site
- (B) LOCATION: 384..391
- (C) IDENTIFICATION METHOD: matinspector prediction

(D) OTHER INFORMATION: name MZF1_C1
score 0.936
sequence AGAGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(410..421)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name SRY_02
score 0.955
sequence GAAACAAAACA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 592..599
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.960
sequence GAAGGGGA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 618..627
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MYOD_Q6
score 0.981
sequence AGCATCTGCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: 632..642
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name DELTAEF1_01
score 0.953
sequence TCCCACCTTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(813..823)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name S8_01
score 0.992
sequence GAGGCAATTAT

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(824..831)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.986
sequence AGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TACTATAGGG CACGGGTSGT CGACGGCCGG GCTGTCTGG AGCAGAGGGC ATGTCAGTAA 60
TGATTGGTCC CTGGGAAGG TCTGGCTGGC TCCAGCACAG TGAGGCATT AGGTATCTCT 120
CGGTGACCGT TGGATTCCTG GAAGCAGTAG CTGTTCTGTT TGGATCTGGT AGGGACAGGG 180

CTCAGAGGGC TAGGCACGAG GGAAGGTCAG AGGAGAAGGS AGGSARGGCC CAGTGAGARG 240
GGAGCATGCC TTCCCCAAC CCTGGCTTSC YCTTGGYMAM AGGGCGKTTY TGGGMACTTR 300
AAYTCAGGGC CCAASCAGAA SCACAGGCCC AKTCNTGGCT SMAAGCACAA TAGCCTGAAT 360
GGGATTTCAG GTTAGNCAGG GTGAGAGGGG AGGCTCTCTG GCTTAGTTTT GTTTTGT TTTT 420
CCAAATCAAG GTAACCTTGCT CCCTTCTGCT ACGGGCCTTG GTCTTGGCTT GTCCTACCC 480
AGTCGGA ACT CCCTACCACT TTCAGGAGAG TGTTTTTAGG CCCGTGGGGC TGTTCGTTC 540
CAAGCAGTGT GAGAACATGG CTGGTAGAGG CTCTAGCTGT GTGCGGGGCC TGAAGGGGAG 600
TGGGTTCTCG CCCAAAGAGC ATCTGCCCAT TTCCACCTT CCCTTCTCCC ACCAGAAGCT 660
TGCTGAGCT GTTTGGACAA AAATCCAAAC CCCACTGGC TACTCTGGCC TGGCTTCAGC 720
TTGGAACCCA ATACCTAGGC TTACAGGCCA TCCTGAGCCA GGGGCTCTG GAAATTCTCT 780
TCCTGATGGT CCTTTAGGT TGGGCACAAA ATATAATTGC CTCTCCCCTC TCCCATTTTC 840
TCTCTTGGGA GCAATGGTCA C 861

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTGGGATGGA AGGCACGGTA

20

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GAGACCACAC AGCTAGACAA

20

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 555 base pairs
 - (B) TYPE: NUCLEIC ACID
 - (C) STRANDEDNESS: DOUBLE
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: promoter
 - (B) LOCATION: 1..500
- (ix) FEATURE:
 - (A) NAME/KEY: transcription start site
 - (B) LOCATION: 501
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 191..206
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name ARNT_01
score 0.964
sequence GGACTCACGTGCTGCT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 193..204
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name NMYC_01
score 0.965
sequence ACTCACGTGCTG
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: 193..204
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name USF_01
score 0.985
sequence ACTCACGTGCTG
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name USF_01
score 0.985
sequence CAGCACGTGAGT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction
 - (D) OTHER INFORMATION: name NMYC_01
score 0.956
sequence CAGCACGTGAGT
- (ix) FEATURE:
 - (A) NAME/KEY: TF binding-site
 - (B) LOCATION: complement(193..204)
 - (C) IDENTIFICATION METHOD: matinspector prediction

- (D) OTHER INFORMATION: name MYCMAX_02
score 0.972
sequence CAGCACGTGAGT
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 195..202
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.997
sequence TCACGTGC
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(195..202)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name USF_C
score 0.991
sequence GCACGTGA
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(210..217)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name MZF1_01
score 0.968
sequence CATGGGGA
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 397..410
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name ELK1_02
score 0.963
sequence CTCTCCGGAAGCCT
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: 400..409
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name CETS1P54_01
score 0.974
sequence TCCGGAAGCC
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1_Q4
score 0.963
sequence AGTGACTGAAC
- (ix) FEATURE:
(A) NAME/KEY: TF binding-site
(B) LOCATION: complement(460..470)
(C) IDENTIFICATION METHOD: matinspector prediction
(D) OTHER INFORMATION: name AP1FJ_Q2
score 0.961
sequence AGTGACTGAAC
- (ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: 547..555
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name PADS_C
 score 1.000
 sequence TGTGGTCTC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

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CTATAGGGCA CGCKTGGTCG ACGGCCCCGG CTGGTCTGGT CTGKTGTGGA GTCGGGTTGA   60
AGGACAGCAT TTGKACATC TGGTCTACTG CACCTTCCCT CTGCCGTGCA CTTGGCCTTT   120
KAWAAGCTCA GCACCGGTGC CCATCACAGG GCCGGCAGCA CACACATCCC ATTACTCAGA   180
AGGAAGTAC GGAATCACGT GCTGCTCCGT CCCCATGAGC TCAGTGGACC TGTCTATGTA   240
GAGCAGTCAG ACAGTGCTTG GGATAGAGTG AGAGTTCAGC CAGTAAATCC AAGTGATTGT   300
CATTCTGTG TGCATTAGTA ACTCCCAACC TAGATGTGAA AACTTAGTTC TTTCTCATAG   360
GTTGCTCTGC CCATGGTCCC ACTGCAGACC CAGGCACTCT CCGGAAGCCT GGAAATCACC   420
CGTGTCTTCT GCCTGCTCCC GCTCACATCC CACACTGTG TTAGTCACT GAGTTACAGA   480
TTTTGCCTCC TCAATTCTC TTGTCTTAGT CCCATCCTCT GTTCCCCTGG CCAGTTTGTC   540
TAGCTGTGTG GTCTC                                     555
  
```

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 63..122
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 15.8
 seq LLLLLLLRHGAQG/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

AACATTTCCT GGAACRSAGA GCGGANSNG NGACAGCGGA GGAVSTGGAT AACAGGGGAC   60
CG ATG ATG TGG CGA CCA TCA GTT CTG CTG CTT CTG TTG CTA CTG AGG   107
Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg
-20 -15 -10
  
```

CAC GGG GCC CAG GGG AAG CCA TCC CCA GAC GCA
 His Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala
 -5 1 5

140

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 285..359
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14
seq LAMLALLSPLSLA/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

ACTAGTTAAA AGTAAGTGGG AAAAGAGTAA ACGCGCGACT CCAGCGCGCG GCTACCTACG 60
 CTGTGTGCTT GCTTTCTCCA GCCATCGGAG ACCAGAGCCG CCCCCTCTGC TCGAGAAAGG 120
 GGCTCAGCGG CGGCGGAAGC GGAGGGGGAC CACCGTGGAG AGCGCGGTCC CAGCCCGGCC 180
 ACTGCGGATC CCTGNAACCA AAAAGCTCCT GCTGCTTCTG TACCCCGCCT GTCCCTCCCA 240
 GCTGCGCAGG GCCCCTTCGT GGGATCATCA GCCCGAAGAC AGGG ATG GAG AGG CCT 296
 Met Glu Arg Pro
 -25
 CTG TGC TCC CAC CTC TGC AGC TGC CTG GCT ATG CTG GCC CTC CTG TCC 344
 Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu Ala Leu Leu Ser
 -20 -15 -10
 CCC CTG AGC CTG GCA CAG TAT GAC AGC TGG CCC CAD KAM CCC GAG TAC 392
 Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa Xaa Pro Glu Tyr
 -5 1 5 10
 TTC CAG CAA CCG 404
 Phe Gln Gln Pro
 15

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 67..120
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.3
seq HILFLLLPVAAA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

AACAGTTCCT CTGGACTTCT CTGGACCACA GTCCTCTGCC AGACCCCTGC CAGACCCAG      60
TCCACC ATG ATC CAT CTG GGT CAC ATC CTC TTC CTG CTT TTG CTC CCA      108
Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro
          -15                      -10                      -5

GTG GCT GCA GCT CAG ACG ACT CCA GGA GAG AGA TCA TCA CTC CCT GCC      156
Val Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala
          1                      5                      10

TTT TAC CCT GGC ACT TCA GGC TCT TGT TCC GGA TGT GGG TCC CTC TCT      204
Phe Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser
          15                      20                      25

CTG CCG CTC CTG GCA GGC CTC GTG GCT      231
Leu Pro Leu Leu Ala Gly Leu Val Ala
          30                      35

```

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 69..134
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.2

seq LALALGLAQPASA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ATTCTCCAT CCTCAGTCTT TGCAAGGCGA CAGCTGTGCC ACCCGGGCTC TGGCAGGCTC   60
CTGGCAGC ATG GCA GTG AAG CTT GGG ACC CTC CTG CTG GCC CTT GCC CTG   110
      Met Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu
            -20                -15                -10

GGC CTG GCC CAG CCA GCC TCT GCC CGC CGG AAG CTG CTG GTG TTT CTG   158
Gly Leu Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu
            -5                1                5

CTG   161
Leu

```

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..122
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.9
seq LVLEFLLSPVEA/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

AAAAACCTG TGGACGCCGA CCCGGGACCG CCGCTGGCTG GCTGCTGCCT CACTCGACCG   60
TC ATG GAG ACC CTG GGG GCC CTT CTG GTG CTG GAG TTT CTG CTC CTC   107
      Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu
            -20                -15                -10

TCC CCG GTG GAG GCC CAG CAG GCC ACG GAG CAT CCG CTG AAG CCG TGG   155
Ser Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp
            -5                1                5                10

CTG GTG GGC CTG GCT GCG GTA GTC GGC TTC CTG TTC ATC GTC TAT TTG   203
Leu Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu
            15                20                25

GTC TTT CTG GCC AAC CGC CTC TGG TGT TCC AAG GCC AGG GCT GAG GAC   251
Val Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp
            30                35                40

```

GAG GAG GAG ACC ACG TTC AGA ATG GAG TCC GGG
 Glu Glu Glu Thr Thr Phe Arg Met Glu Ser Gly
 45 50

284

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3
seq PLLSSLLGGSQA/MD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AACTCACAGC ACGACCAGAG AACAGGCCTG TCTCAGGCAG GGCCTGCGCC TCCTATGCGG 60
 AG ATG CTA CTG CCA CTG CTG CTG TCM TCG CTG CTG GGC GGG TCC CAG 107
 Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln
 -15 -10 -5
 GCT ATG GAT GGG AGA TTC TGG ATA CGA GTG CAG GAG TCA GTG ATG GTG 155
 Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val
 1 5 10 15
 CCG GAG GGC CTG TGC ATC TCT GTN KCC CTG CTC TTT CTC CTA CCC CCG 203
 Pro Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro
 20 25 30
 ACA AGA CTG GAC AGG GTC TAC CCC AGC CGG 233
 Thr Arg Leu Asp Arg Val Tyr Pro Ser Arg
 35 40

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 32..73
 (C) IDENTIFICATION METHOD: Von Heljne matrix
 (D) OTHER INFORMATION: score 10.7
 seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

AACTTTGCCT TGTGTTTTCC ACCCTGAAAG A ATG TTG TGG CTG CTC TTT TTT      52
                               Met Leu Trp Leu Leu Phe Phe
                               -10

CTG GTG ACT GCC ATT CAT GCT GAA CTC TGT CAA CCA GGT GCA GAA AAT      100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
      -5                      1                      5

GCT TTT AAA GTG AGA CTT AGT ATC AGA ACA GCT CTG GGA GAT AAA GCA      148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
      10                      15                      20                      25

TAT GCC TGG GAT ACC AAT GAA GAA TAC CTC TTC AAA GCG ATG GTA GCT      196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
                      30                      35                      40

TTC TCC ATG AGA AAA GTT CCC AAC AGA GAA GCA ACA GAA ATT TCC CAT      244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
                      45                      50                      55

GTC CTA CTT TGC AAT GTA ACC CAG AGG GTA TCA TTC TGG TTT GTG GTT      292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
                      60                      65                      70

ACA GAC CCT TCA AAA AAT CAC ACC CTT CCT GCT GTT GAG GTG CAA TCA      340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
                      75                      80                      85

GCC ATA AGA ATG AAC AAG AAC CGG ATC AAC AAT GGC TTC TTT CTA AAT      388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
                      90                      95                      100                      105

GAC CAA ACT CTG GAA TTT TTA AAA ATC CCT TCC ACA CTT GCA CCA ACC      436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Thr
                      110                      115                      120

CGG
Arg
                                         439

```

(2) INFORMATION FOR SEQ ID NO: 45:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 20..100
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.7
seq LPLLCLFLQGATA/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
AGAGATCGCA GCCCAACCC ATG GCC GGG TCT CCT AGC CCC GCC GCG GGC CGG      52
      Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg
                -25                      -20

CGA CTG CAG CTT CCC CTG CTG TGC CTC TTC CTC CAG GGC GCC ACT GCC      100
Arg Leu Gln Leu Pro Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala
      -15                      -10                      -5

GTC CTC TTT GCT GTC TTT GTC CGC TAC AAC CAC AAA ACC GAC GCT GCC      148
Val Leu Phe Ala Val Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala
      1                      5                      10                      15

CTC TGG CAM CGG AAG CTT GGG
Leu Trp Xaa Arg Lys Leu Gly
                20                      169
```

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 40..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.6
seq ALALLLVLP LLWP/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

ACTGCCCTGC CCTGGCCTGA CCCAGGCCT AQTGAGTCC ATG AAA TGG CCC TGG      54
                               Met Lys Trp Pro Trp
                               -35

ACC TGC CTT GCC ATC CTC TGT CCT GGC CCT GTA TTG TCC CCA CCA TGC      102
Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val Leu Ser Pro Pro Cys
          -30                -25                -20

TCT GGT CCA RCG CTT GCC CTA GCC CTG TTG CTA GTC CTG CCA CTG CTA      150
Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu Val Leu Pro Leu Leu
          -15                -10                -5

TGG CCC TGC TCT GTT TTT GGC CAT GCC CTG TGC TAM CCT AGC CCT GCC      198
Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys Xaa Pro Ser Pro Ala
          1                5                10

CGA AGG                                204
Arg Arg
15

```

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 28..96
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10
seq PLLGLLLSLPAGA/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

AACCGAGCTG GATTTGTATG TTGCACC ATG CCT TCT TGG ATC GGG GCT GTG ATT      54
                               Met Pro Ser Trp Ile Gly Ala Val Ile
                               -20                -15

TTT CCC CTC TTG GGG CTG CTG CTC TCC CTC CCC GCC GGG GCG GAT GTG      102
Leu Pro Leu Leu Gly Leu Leu Leu Ser Leu Pro Ala Gly Ala Asp Val
          -10                -5                1

AAG GGT CGG AGC TGC GGA GAG GTC CGC CAG GCG TAC GGT GCC AAG GGA      150
Lys Ala Arg Ser Cys Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly
          5                10                15

```

```

TTC AGC CTG GCG GAC ATC CCC TAC CAG GAG ATC GCA KGG GAA CAC TTA      198
Phe Ser Leu Ala Asp Ile Pro Tyr Gln Glu Ile Ala Xaa Glu His Leu
   20                25                30

AGA ATC TGT CCT CAG GAA TAT ACA TGC TGC ACC ACA GAA ATG GAR GAC      246
Arg Ile Cys Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp
   35                40                45                50

AAG TTA AGC CAA CAA AGC AAA CTC GAA TTT GAA AAC CTT GTG GAA GAG      294
Lys Leu Ser Gln Gln Ser Lys Leu Glu Phe Glu Asn Leu Val Glu Glu
                55                60                65

ACA AGC CAT TTT GTG CGC ACC ACT TTT GTG TCC AGG CAT AAG AAA TTT      342
Thr Ser His Phe Val Arg Thr Thr Phe Val Ser Arg His Lys Lys Phe
                70                75                80

GAC GGT AGG
Asp Gly Arg
   85

```

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 99..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10
seq LWLSLLVPSCLCA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

ACCACTGTGC CCAGCCATTG TCTATACAGT TTGAATAACA CACTGAAAAA ACAGATCAGT      60
GCATATCTTC CACAATTAAC AATGCATTG TTTAGAGC ATG TTG CTG CAT TGG GTG      116
                Met Leu Leu His Trp Val
                -25

CGC TCT CAG GMT GDC AGC GAC KCN AAG CTT TGG TTG AGT TTG CTA GTG      164
Arg Ser Gln Xaa Xaa Ser Asp Xaa Lys Leu Trp Leu Ser Leu Leu Val
   -20                -15                -10

CCA AGT TGT TTA TGT GCC TCC CCT TGG CCC CTT CCT TCC CTG CCA CTC      212
Pro Ser Cys Leu Cys Ala Ser Pro Trp Pro Leu Pro Ser Leu Pro Leu
   -5                1                5                10

```

CTT CTT CCT CCC AGC TTG CTG AGC TTG CTG
 Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu
 15 20

242

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 122..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6
seq LLLFSLLVSPPTC/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAACTCTT TCTTCGGCTC GCGAGCTGAG AGGAGCAGGT AGAGGGGCAG AGGCGGGACT 60
 GTCGTCTGGG GGAGCCGCCC AGGAGGCTCC TCAGGCCGAC CCCAGACCCT GGCTGGCCAG 120
 G ATG AAG TAT CTC CGG CAC CGG CGG CCC AAT GCC ACC CTC ATT CTG GCC 169
 Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 -30 -25 -20
 ATC GGC GCT TTC ACC CTC CTC CTC TTC AGT CTG CTA GTG TCA CCA CCC 217
 Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
 -15 -10 -5
 ACC TGC AAG GTC CAG GAG CAG CCA CCG GCG ATC CCC GAG GCC CTG GCC 265
 Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
 1 5 10
 TGG CAC ACT CCA CCT ACC CGA TGG 289
 Trp Xaa Thr Pro Pro Thr Arg Trp
 15 20

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 26..130
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.5
seq AMWWLLWGVQA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

GCAGGTCCCA GATGTCCAST TCCAG ATG CCT GGA CCC AGA GTG TGG GGG AAA      52
                               Met Pro Gly Pro Arg Val Trp Gly Lys
                               -35                               -30

TAT CTC TGG AGA AGC CCT CAC TCC AAA GGC TGT CCA GGC GCA ATG TGG      100
Tyr Leu Trp Arg Ser Pro His Ser Lys Gly Cys Pro Gly Ala Met Trp
-25                               -20                               -15

TGG CTG CTT CTC TGG GGA GTC CTC CAG GCT TGG CCA AMC CCG GGG CTC      148
Trp Leu Leu Leu Trp Gly Val Leu Gln Ala Trp Pro Xaa Pro Gly Leu
-10                               -5                               1                               5

CGT CCT CTT GGC CCA AGA GCT ACC CCA GCA GCT GAC ATC CCC CGG GTA      196
Arg Pro Leu Gly Pro Arg Ala Thr Pro Ala Ala Asp Ile Pro Arg Val
10                               15                               20

CCC AGA GCC GTA TGG CAA AGG CCA AGA GAG CAG CAC GGA CAT CAA GGC      244
Pro Arg Ala Val Trp Gln Arg Pro Arg Glu Gln His Gly His Gln Gly
25                               30                               35

TCC AGA GGG CTT TGC TGT GAG GCT CGT CTT CCA GGA CTT CGA CCT GGA      292
Ser Arg Gly Leu Cys Cys Glu Ala Arg Leu Pro Gly Leu Arg Pro Gly
40                               45                               50

GCC GTC CCA GGA CTG TGC AGG GGA CTC TRW BAC AAT CTC ATT CGT CGG      340
Ala Val Pro Gly Leu Cys Arg Gly Leu Xaa Xaa Arg Leu Ile Arg Arg
55                               60                               65                               70

TTC GGA TCC AAG CCA GTT CTG TGG TCA GCA AGG CTC CCC TCT GGG CAG      388
Phe Gly Ser Lys Pro Val Leu Trp Ser Ala Arg Leu Pro Ser Gly Gln
75                               80                               85

GCC CCC TGG TCA GAG GGA                                          406
Ala Pro Trp Ser Glu Gly
90

```

(12) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 62..172

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.2
seq LLAVLLASWRLWA/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

AACTGGTGCG GCCGAGTGAC AGTTGACCGG TTTTAACCAA GTGACTGGTT CTAGCCACGT    60
T ATG TGC GGC CCA GCC ATG TTC CCT GCC GGT CCT CCG TGG CCC AGA GTC    109
Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
   -35                               -30                               -25

CGA GTC GTG CAG GTG CTG TGG GCC CTG CTG GCA GTG CTC CTG GCG TCG    157
Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
   -20                               -15                               -10

TGG AGG CTG TGG GCG ATC AAG GAT TTC CAG GAA TGC ACC TGG CAG GTT    205
Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
   -5                               1                               5                               10

GTC CTG AAC GAG TTT AAG AGG GTA GGC GAG AGT GTC GTG AGC GAC AST    253
Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
      15                               20                               25

TCT TTG AGC AAG AGC CCG GGG    274
Ser Leu Ser Lys Ser Pro Gly
      30

```

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 71..235

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.2

seq SLLLLSTALNILA/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

ACATATCTTT GCAATTGTGA ACATTCAATC ATTTTCAACA CACGTTTCATG GTTAATATTT    60
CTAGGAAACT ATG CAT AGA AGA AAA CTT CCT TTA ACC AAT AAA AGG CAA    109
      Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln
      -55                -50                -45
CTT CAA AAA MCA TTG AGT AAA TTC ATA TTC AGT GAT GAA TTG TTT AGA    157
Leu Gln Lys Xaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg
      -40                -35                -30
AAT ATT CTC TTT AGT TTA AGA ACA TTA AGG ATG ATA CTA TCA CTA CTT    205
Asn Ile Leu Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu
      -25                -20                -15
CTG TTG AGC ACT GCA TTG AAT ATC TTA GCC TGC CAA ATA AAT GAA GAA    253
Leu Leu Ser Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Glu
      -10                -5                1                5
CTG GGG
Leu Gly
259

```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 182..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.3
seq VSALLNANFGVLS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

AAAACGCCGG GAGCTGCGAG TGTCCAGCTG CGGAGACCCG TGATAATTCTG TTAACATAAT    60
CAACAAACGG GACCCCTTCTG TGTGCCAGAA ACCGCAAGCA GTTGCTAACC CAGTGGGACA    120
GGCGGATTGG AAGAGCGGGA AGGTCCTGSC CCAGAGCAGT GTGACACTTC CCTCTGTGAC    180
C ATG AAA CTC TGG GTG TCT GCA TTG CTG ATG GCC TGG TTT GGT GTC CTG    229
Met Lys Leu Trp Val Ser Ala Leu Met Ala Trp Phe Gly Val Leu
      -15                -10                -5

```

AGC TGT GTG CAG GCC GAD HYG
 Ser Cys Val Gln Ala Xaa Xaa
 1 5

250

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1
seq LCLVCLLVHTAFR/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

| | |
|--|-----|
| AAGAGCCTGT GCTACTGGAA GGTGGCGTGC CCTCCTCTGG CTGGTACC ATG CAG CTC | 57 |
| Met Gln Leu | |
| CCA CTG GCC CTG TGT CTC GTC TGC CTG CTG GTA CAG ACA GCC TTC CGT | 105 |
| Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr Ala Phe Arg | |
| -15 -10 -5 | |
| GTA GTG GAG GGC CAG GGG TGG CAG GCG TTC AAG AAT GAT GCC ACG GAA | 153 |
| Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp Ala Thr Glu | |
| 1 5 10 15 | |
| ATC ATC CCC GAG CTC GGA GAG TAC CCC GAG CCT CCA CCG GAA CGG | 198 |
| Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro Glu Arg | |
| 20 25 30 | |

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 99..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq ILLCSVAVXLSPS/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

CATAGGGTTT CGAAAATTAT CCACACTTTC TATGGTAATA GAATCTGATA TGGTTCAC TC      60
TTGGTGTGTG ACATTCTGTG GGTCTGGGTA AATGTATA ATG ATA TGT ATC CAC CAN    116
                               Met Leu Cys Ile His Xaa
                               -30
KAT AGG ATC ATA CAG GAC AGT TTC ATT GCC CTA AAA ATT CTC TTA TGT      164
Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala Leu Lys Ile Leu Leu Cys
-25                -20                -15                -10
TCT GTC GCT GTA TSM CTG TCT CCC TCC GAC CCC CTG GCG CCG              206
Ser Val Ala Val Xaa Leu Ser Pro Ser Glu Pro Leu Ala Pro
                -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 8..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LPFLSLFWPWAPG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

AAGGAGC ATG GGT GGT TTT TTT CCC CCT ACC GAG GTC CGT GAG GTG TGT      49
Met Gly Gly Phe Phe Pro Pro Thr Glu Val Arg Glu Val Cys
                -35                -30                -25
GCT AAC CAA GGG GCG GCT CAC AAC CGT GAC AGA CTG CCA TTC CTG AGT      97
Ala Asn Gln Gly Ala Ala His Asn Arg Asp Arg Leu Pro Phe Leu Ser
                -20                -15                -10

```

```

CTC TTC TGG CCA TGG GCC CCC GGA GCC GTG AGC GTC GGG CAG GCG CGG      145
Leu Phe Trp Pro Trp Ala Pro Gly Ala Val Ser Val Gly Gln Ala Arg
      -5              1              5

TAC AGA ACA CCA ACG ACA KSA GCG CCC TCA GCA ACC GTT CCC TGG CCG      193
Tyr Arg Thr Pro Thr Thr Xaa Ala Pro Ser Ala Ser Val Pro Trp Pro
      10              15              20

CGC GCG GGT ACG TGC AGG ACC CCT ACG                                  220
Arg Ala Gly Thr Cys Arg Thr Pro Thr
      25              30

```

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 21..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq HLWILLLLSFCWM/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

ACTTCCCTAT TATTCCTGAA ATG AAA TTA TTT TAC AAC CAG CTC GTT TCA GAA      53
      Met Lys Leu Phe Tyr Asn Gln Leu Val Ser Glu
      -30              -25              -20

ACA AAA CAT GAT TTT GCA CAT TTG TGG ATT TTG TTG TTA TTC TCA TTT      101
Thr Lys His Asp Phe Ala His Leu Trp Ile Leu Leu Leu Phe Ser Phe
      -15              -10              -5

TGT TGG ATG TCT AGA AGC TTT TTT TTT TTT                                  131
Cys Trp Met Ser Arg Ser Phe Phe Phe Phe
      1              5

```

(2) INFORMATION FOR SEQ ID NO: 58:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 111..170
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLFFHILFHSCFS/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

ACCTTTAAGA TTACCTGTAT AATAAATGTG TGCAGACACC ATCCAAAAAG GTGTAAAAAA   60
TTGCAAAGGA AAAATAAATA CTGGCCAACA CAGTGTCTTT AAAAGTACCC ATG CCT   116
                                     Met Pro
                                     -20
AGT GAG TCC CCT CCC TTG CTG TTC TTT CAC ATT CTC TTC CAT AGC TGT   164
Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His Ser Cys
      -15                      -10                      -5
TTC TCC CAC CTC TTG
Phe Ser His Leu Leu
      1

```

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 18..221
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLCSALAWQQSLS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ATAAACAGGA AAGCACT ATG TCT TCA ATG TGG TCT GAA TAT ACA ATT GGT   50
      Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly
      -65                      -60
GGG GTG AAG ATT TAC TTT CCT TAT AAA GCT TAC CCG TCA CAG CTT GCT   98

```

Gly Val Lys Ile Tyr Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala
 -55 -50 -45

ATG ATG AAT TCT ATT CTC AGA GGA TTA AAC AGC AAG CAA CAT TGT TTG 146
 Met Met Asn Ser Ile Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu
 -40 -35 -30

TTG GAG AGT CCC ACA GGA AGT GGA AAA AGC TTA GCC TTA CTT TGT TCT 194
 Leu Glu Ser Pro Thr Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser
 -25 -20 -15 -10

GCT TTA GCA TGG CAA CAA TCT CTT AGT GGG AAA CCA GCA GAT GAG GGC 242
 Ala Leu Ala Trp Gln Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly
 -5 1 5

GTA AGT GAA AAA GCT GAA GTA CAA TTG TCA TGT TGT TGT GCA TGC CAT 290
 Val Ser Glu Lys Ala Glu Val Gln Leu Ser Cys Cys Cys Ala Cys His
 10 15 20

TCA AAG GAT TTT ACA AAC AAT GAC ATG AAC CAA GGA ACT TCA CGT CAT 338
 Ser Lys Asp Phe Thr Asn Asn Asp Met Asn Gln Gly Thr Ser Arg His
 25 30 35

TTC AAC TAT CCA AGC ACA CCA CGG 362
 Phe Asn Tyr Pro Ser Thr Pro Arg
 40 45

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 19..102
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq EVRFLGFVSCLOS/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TAGCTATTTT CAGCGCTT ATG GCT CTG TTC TTG GAG TTA TTT CTA AAT TCT 51
 Met Ala Leu Phe Leu Glu Leu Phe Leu Asn Ser
 -25 -20

TAT TCT CTT TTG TTT GTA AGG TTT CTT GGC TTT GTT TCC TGT TTG CAG 99
 Tyr Ser Leu Leu Phe Val Arg Phe Leu Gly Phe Val Ser Cys Leu Gln
 -15 -10 -5

TCT GAT CCC ATT TGC TCT TTT TTT TTT TTT
Ser Asp Pro Ile Cys Ser Phe Phe Phe Phe
1 5

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 114..185
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq LMAGSSLSAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

| | | | | | | |
|---|---|------------|------------|------------|----------------|-----|
| ATACCTTCAAA | TCTTGAATTA | AATGAAGAAA | TTTATTTTAC | TGATTCTCTT | GAAATAAAGA | 60 |
| GAAATGAAAA | TTTTCCAAAG | GATTATGTGA | AATTTTCAGA | TAAAGAAGAA | TTT ATG Met | 116 |
| AAT GAA GAT GAG AAG GAA ATG AAG GAA ATT CTA ATG GCA GGA AGT AGT | Asn Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser Ser | -20 | -15 | -10 | | 164 |
| TTA TCA GCT GGA GTT AGT GGG GAA GAT AAA ACC GAG ATA TTG AAT CCC | Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn Pro | -5 | 1 | 5 | | 212 |
| ACT CCA SCG ATG GCC AAA TCT CTG ACC ATA GAC TGT CTG GAA TTG GCA | Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu Ala | 10 | 15 | 20 | 25 | 260 |
| TTA CCC CCT GAA CTG GCT TTT CAA CTT AAT GAA TTA TTT GGT CCT GTT | Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro Val | 30 | 35 | 40 | | 308 |
| GGT ATT GAT TCA GGG TCT CTA | Gly Ile Asp Ser Gly Ser Leu | 45 | | | | 329 |

(2) INFORMATION FOR SEO ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq IIPLIXXLSLCLC/LW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

CTATACGTGA TAAGTGAATA AAATGTGTCA GAGTGTACTA CTTAGAATTT TCATAGATTG   60
TAAAGATTTT CTATATATTT ATTTGAATTG GTAATTGGTT ATTAGCAGTT TGGTGTAGCT  120
GTTTTTAATT GTACAACAAT TAAGATATCA CCTATATTCT CGAAGA ATG GGA TCA   175
                               Met Gly Ser
                               -20

TTC CTT CTA GGA GGG ATT ATC CCT TTA ATA NNT TTN CTT TCT CTT TGT   223
Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu Ser Leu Cys
   -15                               -10                               -5

CTT TGT TTA TGG TGG AGA ATA ATT   247
Leu Cys Leu Trp Trp Arg Ile Ile
    1                               5

```

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 277..369
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq VCLLCSGCSCAWS/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ACGAGTGTTA CAGAGGAGAT CTGGTTTCTG GAGGTCTCCA GGATGGGGCT GTAGCCTAAA   60
AGGAAGACTA TGTGAGGCAG CAGGCAAGCA GCAGCAAGTG GAAAGGCTTG GAGATGTGGA   120
GGACGTTATA TGGTACTCAG AGAGCAGCAG TACATGGATG GCAAGTGTGG CGTTGTGCTG   180
CCACCCACTT CCCCATGCCA AAAGCATATA ACTGCTAATC ASTTACCGCA TTTTGTGCTG   240
CCGAATTCGT AAGCAGCCCC AAGAGTTCTC AACAGG ATG CTT CAG GTG GCC ACT   294
                               Met Leu Gln Val Ala Thr
                               -30
ACT AAT TAT TTG GAG TTG GCA CGT GAG GTT AAA CCT GTT TGT CTT CTT   342
Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val Lys Pro Val Cys Leu Leu
-25                -20                -15                -10
TGT AGT GGG TGT TCC TGT GCC TGG AGC GTA GGA TGT GTG TKG GAG TCG   390
Cys Ser Gly Cys Ser Cys Ala Trp Ser Val Gly Cys Val Xaa Glu Ser
                -5                1                5
GAG TCA GAA   399
Glu Ser Glu
    10

```

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 175..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
seq PFFLALCFPKSTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

```

ATTACTTTGT CTAGATCAGG AGATGCTAGT ATATTCTTAG CACTAAGACC CCTCTGAAAT   60
CTTGTCCAAC ATTTAGCCAC CCAGRAGTTG TKCTTTACTA CACCTTTGAG GGTTATGCCC   120
TGTACATGTG CAGCTTAGGG GTTCAAGGAC AATCTCTTTA CACATTTTGT GGTT ATG   177
                               Met

```

TTC TGT CTA GCT CCT TTC TTT TTA GCA CTC TGC TTC CCA AAA TCT ACC 225
Phe Cys Leu Ala Pro Phe Phe Leu Ala Leu Cys Phe Pro Lys Ser Thr
-15 -10 -5

TCA CAG CCC CAA AGG
Ser Gln Pro Gln Arg
1

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 240..335
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..96
id AA270737
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 236..331
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.5
seq QCLLCISPPVFC/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

| | | | | | | |
|---|-------------|------------|------------|------------|------------|-----|
| TCTCTTTTGC | TGTTTTTCATC | AAGATAGTAG | AGCACATCTT | CTTCTCACAG | ACTACAAC | 60 |
| TGTGGTTTCAG | CACGAGGCAG | TAGAGGAAAG | TGCCTCGACT | GTGGGAGGCT | TGGSCAARAT | 120 |
| CCAAAGACTT | TCTCTCCTTG | TIGCTGGAGT | CGCTAAAAGA | ACAGTTTAAT | AATGCCACAC | 180 |
| CCATCCCCAC | CCACAGTTGT | CCCCTATCTC | CAGACCTCAT | TCCCAATGAA | GTAGA ATG | 238 |
| | | | | | Met | |
| TCT GAA AGC AGA TTT CAA CCA CAG AAT CAA GGA GGT TCT CTT CAA CTC | | | | | | 286 |
| Ser Glu Ser Arg Phe Gln Pro Gln Asn Gln Gly Gly Ser Leu Gln Leu | | | | | | |
| -30 | | -25 | | -20 | | |
| CCT CTT CAG TGC CTA CTA TGT TGC ATT TCT CCC CCT GTG TTT TGT GAA | | | | | | 334 |
| Pro Leu Gln Cys Leu Leu Cys Cys Ile Ser Pro Pro Val Phe Cys Glu | | | | | | |
| -15 | | -10 | | -5 | | 1 |

```

GST AAC TGG TTA TCT TAC TTT TAT GTG CTT CCT GGA TTT GTG TGT GAA   382
Gly Asn Trp Leu Ser Tyr Phe Tyr Val Leu Pro Gly Phe Val Cys Glu
      5              10              15

TTA CAT AAA CTG GGT ATT TCT TGT TTA ATC CCC CTT TTC TCT GTC TCC   430
Leu His Lys Leu Gly Ile Ser Cys Leu Ile Pro Leu Phe Ser Val Ser
      20              25              30

CCT TTG GCA GCC TGG ATG GTG   451
Pro Leu Ala Ala Trp Met Val
      35              40

```

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq SSCLLGLLHLSSQ/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

```

ATGGAGCAGA GGTCCAGCTG TGGTGAGGAT TGGCACAGTC GTGCTTGTGG SACTCCTCCT   60
TGSTCCAACT CTAATGCTCA ACCTACACCA TCACCCCTGT GCTTGCTCCT CTA ATG   116
                                     Met

CCT AAG CAC TGT CAT TCC TTT ATC ACT AGT AGT TGC CTG TTG GGT TTG   164
Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly Leu
      -20              -15              -10

CTC CAT TTG TCC TCA CAG TTT AGC TGC CCT GGA AGG AAA CTC CAC CCT   212
Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His Pro
      -5              1              5              10

GCT CAG AGA CAC ACT GAG GCT GAG ACC CAA GGG AUG CCC CTC TCT GAC   260
Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser Asp
      15              20              25

AGG   263
Arg

```

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 166..222
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq FIXEPLLEPFSEFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

ATCTCTCCTT TTTTCTGTA ACTGTGCTGG TTTTGTTTTG GTCTTCCTCT CATACCCGTT   60
TCTGCATTTC ATCTTTTCTT TCTATTGTA CTCATTTCAT TTTTTTTTTT AACCTTATCT   120
TTTGTTCCTC TTGTTTATCC CATCCTTTTT GATAAAATCC ATCGC ATG TGT CTT CTT   177
                               Met Cys Leu Leu
TTT TYC TTT ATT TYC TTT CCT TTC CTT TTY CCT TTT TCT TTC TCC CAA   225
Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe Ser Phe Ser Gln
-15                               -10                               -5                               1
ACT TTT TCC TTT TCA CAG CAT TGG AAC ACG GGA GGT AGT CAC CCA GAA   273
Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly Ser His Pro Glu
      5                               10                               15
GAA CTT GAG CGG CCT GGT GCC CAT CCG AGA CTT AAG GCT AGA CCC CAG   321
Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys Ala Arg Pro Gln
      20                               25                               30
CCT CCT CTG TTC CAT CCC TTT ATT AGC TCT                               351
Pro Pro Leu Phe His Pro Phe Ile Ser Ser
      35                               40

```

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 30..104
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LLVASGHAEGVSA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

ACGCGCAGAC CCAGCGCCGA GCGCGAGCC ATG GCG TCC GAG CGG MTC CCT AAY      53
               Met Ala Ser Glu Arg Xaa Pro Asn
               -25                      -20

AGG CCC GGC TGT CTG CTC GTR GCC AGC GGC GMC GCC GAR GGT GTG TCG      101
Arg Pro Xaa Cys Leu Leu Val Ala Ser Gly Xaa Ala Glu Gly Val Ser
      -15                      -10                      -5

GCC CAG TCC TTC CTC CAS TGT TTC ACG ATG GCC AGC ACC GSC TTC AAC      149
Ala Gln Ser Phe Leu Xaa Cys Phe Thr Met Ala Ser Thr Xaa Phe Asn
      1                      5                      10                      15

CTG CAG GTG GCC AYC CCT GKG GGG AAA GCC ATG GAA TTT GTS GAT GTG      197
Leu Gln Val Ala Xaa Pro Gly Gly Lys Ala Met Glu Phe Val Asp Val
      20                      25                      30

ACT GAS AGC AAT GCA CGC TGG GTG CAA GAC      227
Thr Xaa Ser Asn Ala Arg Trp Val Gln Asp
      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 160..234
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LAFQLVFLRATSG/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

AATTTCAAGT TGTGATAAAA GTTCAGACAA CCATCACTGG ACCTACAGAT TGAGTGATTA      60

```

TTATAGTGGG GATGTCCTTG GGTTAGTAAG CCTAAAGGAA GTAATTTCTG TTAAAGGAGA 120

TGTTAGTGGC CATTGTCATC TTAATGTCAA TCTTATCAG ATG TTC CCA GAC TAC 174
Met Phe Pro Asp Tyr
-25

AAA CTG GGT GGG TCA TAT CTC TTA GCA TTT CAA CTG GTA TTT CTC AGA 222
Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln Leu Val Phe Leu Arg
-20 -15 -10 -5

GCA ACT AGT GGC TCA TGT TCC AAA TAT AGA AGG CAT TTG CAT AAC ATC 270
Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg His Leu His Asn Ile
1 5 10

AAT GTT AGA CCT GGG CTT GTT AGA CTC TTG GGC TCA TGT ATA CAA AAG 318
Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly Ser Cys Ile Gln Lys
15 20 25

CAA CCT GGG 327
Gln Pro Gly
30

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 44..118
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLLXLNLLLLIALE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

AAATGTGTAC ACGCCCAGCT TCCTGCCTGT TACTCTCCAC AGT ATG CGA AGA ATA 55
Met Arg Arg Ile
-25

TCC CTG ACT TCT AGC CCT GTG CGC CTT CTT TTG TDT CTG CWG TTR CTA 103
Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa Leu Xaa Leu Leu
-20 -15 -10

CTA ATA GCC TTG GAG ATC ATG GTT GGT GGT CAC TCT CTT TGC TTC AAC 151
Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn
-5 1 5 10

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 215..292
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq EMFLVLLVTGVHS/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

AAAAAGTACT GAGAGGTTGA TGGGACTGTT CGATTAGCTC CTCGAGAAG AAGAGAAAAG   60
GTTCTTGGAC CTCTCCCTGT TTCTTCCTTA GAATAATTG GATGGGATTT GTGATGCAGA  120
AAAGCCTAAG GGAAAAAGAA TATTCATTCT GTGTGGTGAA AATTTTTTGA AAAAAAATT  180
GCCTTCTTCA AACAAGGGTG TCATTCTGAT ATTT ATG AGG ACT GTT GTT CTC ACT   235
                               Met Arg Thr Val Val Leu Thr
                               -25                               -20

ATG AAG GCA TCT GTT ATT GAA ATG TTC CTT GTT TTG CTG GTG ACT GGA   283
Met Lys Ala Ser Val Ile Glu Met Phe Leu Val Leu Leu Val Thr Gly
                               -15                               -10                               -5

GTA CAT TCA AAC AAA GAA ACG GCA AAG AAG ATT AAA AGG CCC GGG       328
Val His Ser Asn Lys Glu Thr Ala Lys Lys Ile Lys Arg Pro Gly
                               1                               5                               10

```

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 150..269
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq ISLLFIFFSIANS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ATTCTTTCCT TCTCATATCT ACAATTGCTC CTTTCTAGTT CAGTTCCTA GTACAGCTGG      60
AGTGATTATT KSKKTTAAA AAATGCAAGC ATAAAAAGA AATAACAAA TAGTTAAATC      120
ATGTTATTCT TTTGTTTACA CTGTAATGA ATG TCT TCC CCA TTG CTT GTA GAA      173
                               Met Ser Ser Pro Leu Leu Val Glu
                               -40                               -35
CAA AGT TCT ACA AAG TCT CCC AAA AGC TGG TCC TGG TCC TTT CTA GCT      221
Gln Ser Ser Thr Lys Ser Pro Lys Ser Trp Ser Trp Ser Phe Leu Ala
      -30                               -25                               -20
TTC TCT TGC ATA AGT CTT CTT TTT ATT TTT TTC AGC ATT GCA AAT TCT      269
Phe Ser Cys Ile Ser Leu Leu Phe Ile Phe Phe Ser Ile Ala Asn Ser
      -15                               -10                               -5
TCC CCC TGC GGG
Ser Pro Cys Gly
1

```

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 96..170
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq IPLLLLFHLSFL/NS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

AGAACAAAGT TTAGAATGAT ATGTTTATGC CTGTGACAT TTATCTTGTT AGATTATGCT      60
CACTAAGCCA TTGGGGTGTG TGGGGAATTT GATCA ATG TAT CTT TTC TGT CTC      113

```

Met Tyr Leu Phe Cys Leu
 -25 -20

TTT TCA GTT TCG AAA ACT ATC CCT CTG CTG CTG CTT TTC TTC CAC TTG 161
 Phe Ser Val Ser Lys Thr Ile Pro Leu Leu Leu Leu Phe Phe His Leu
 -15 -10 -5

TCT TTT CTC AAT AGC TTG 179
 Ser Phe Leu Asn Ser Leu
 1

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 170..217
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq CLLILKFLSPAET/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

ACAGAGTTCA CTTCTAGGAT ATTCTTCCC AATCTTCACA GTCACCTCAT AGTCACTATG 60

AGGATTACAT GAGTKAATAT TTGTAAAAAG CGTTCAGGAG AGTGCTTGCT TCACATCAAA 120

TACTATATAT ACTTGTTAAA TAAATAGATC TCATTACCCC CACGAAACA ATG ATC GTT 178
 Met Ile Val
 -15

TGT CTC CTG ATT CTC AAG TTT TTG TCT CCA GCA GAG ACB TCT ATT CTG 226
 Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr Ser Ile Leu
 -10 -5 1

AGC TCC ATA GCT ACA TAT GGG GCT TTT TAT TTC ATA GTT CCA CTG GAG 274
 Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val Pro Leu Glu
 5 10 15

GTT TCA CAA ATC CTT CAA ACT CAG 298
 Val Ser Gln Ile Leu Gln Thr Gln
 20 25

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 180..254
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LILCFILFHTHT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```
ACAAACTGGT TACCCTGCCA CATGTATACC CCCTTCTCCC CATTCTCACT TCCTCGTTAG   60
ACGAAATGAT CATCCAGTGA AGCCATAGAT TATATTGGCC ATCTAATATC AAACCATATT  120
GGTCTCATT T GAAAATCTTT CATGATGCTT TGTGGTATTC ACAGTGAAGT TTAGATTCC   179
ATG GAT AAG AGC ATC AAG TCC TCT ATA ATC TGG TCT CTG ATT CTC TGT   227
Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys
-25          -20          -15          -10
TTT CTT TTT ATC CTG CAC ACA CAC ACA CAC ACA CAC ACA CAC ACA CAC   275
Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His Thr His
          -5              1              5
```

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 283..390
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq IFDLLLLLXXSNQ/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

ACAGACCTCT TTGAAAATCT AATGAGAGCC ATAGACTTCA CCCTAAAAAA ATATATATGC   60
ATAAAAAGTT TAAATATAGT TTGGAGAGTA ACGCACCTTC CCCTAAAGCA ATTCCTAAAC  120
CTCATTTAAA GGATCTATAT TCTATAGTTC AGTTCTGCAT TTTTAATGTC TTCTATATTG  180
TCTCATGCTA GAATAGTCAT TATATCTTCA TATGTAATAT TTTAAGTGTG AATTATCATC  240
TAACACTTCC TGTCTTCTGT CCCCCAAATC TATACTTCTC CC ATG TTC TTT ATT   294
                                   Met Phe Phe Ile
                                   -35

TTC ATT AAT GGC TTT ACW CTC CTT CTA ATG ACC CTA GCC ATG AAA CCC   342
Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu Ala Met Lys Pro
      -30                      -25                      -20

AGG CAT CCT ATT TTT GAC CTC TTG CTA TTG CTK RAS HTA TCT AAT CAA   390
Arg His Pro Ile Phe Asp Leu Leu Leu Leu Xaa Xaa Ser Asn Gln
      -15                      -10                      -5

TTG CCA GTT ACG GGG                                           405
Leu Pro Val Thr Gly
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 3..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LWPFLTWINPALS/IC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

AC ATG TGC CCT AGT CTG GAA GAG GCT CCC AGT GTC AAG GGG ACT CTG   47
Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu
      -60                      -55                      -50

CCC TGC TCA GGA CAA CAG CAG CCT TTC CCG TTT GGA GCC TCA AAC ATC   95
Pro Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile

```

| | | | | |
|---|-----|-----|-----|--|
| -45 | -40 | -35 | -30 | |
| CCA CTA CTC CTG GGC AGG AGC AGA AAG GTG GCT CGA GGT GCA CCG GTC | 143 | | | |
| Pro Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val | | | | |
| -25 | -20 | -15 | | |
| CTG TGG CCA TTT CTC ACT TGG ATA AAC CCT GCA CTG TCC ATC TGT GAC | 191 | | | |
| Leu Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp | | | | |
| -10 | -5 | 1 | | |
| CCC TTA GGA TCC TGC GGA TGG CAG | 215 | | | |
| Pro Leu Gly Ser Cys Gly Trp Gln | | | | |
| 5 | 10 | | | |

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 287..337
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSALWFCHPCCL/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

| | |
|---|-------------|
| AAGCTCCAAG GCAGGAAGAG AATTGGGCAT CGGGTACGAA CCTGGCAGCT CAGGAGTCGG | 60 |
| GGCTCCACTC ACCCCACACA AAAAGATGAA AAAAGCGCAW AGAGCTCAAT GCATTGATTG | 120 |
| GTTTGGCTGG GGACAGCCGG AGAAAGAAGC CCAAGAAAGG CCCAAGCACT CACCGCCTGC | 180 |
| TTCGCACTGA GCCTCCCGAC TCATACTCTG AGTCCAGCTC CAAAGAGGAA GAGGAATTCG | 240 |
| GTGTGGTTGG AAATCGCTCT CGCITTGCCA AGGGAGACTA TTTACG ATG CTG CAA | 295 |
| | Met Leu Gln |
| | -15 |
| GAT CTG TTA TCC GCT CTG TGG TTT TGT CAT CCT TGC TGC CTG TGT TGT | 343 |
| Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys Leu Cys Cys | |
| -10 | -5 |
| | 1 |
| GGC CTG TGT TGG CTT GGT GTG GAT GCA GGT TGC TCT CAA GGA GGA TCT | 391 |
| Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln Gly Gly Ser | |
| 5 | 10 |
| | 15 |

GGA TGC CCG
Gly Cys Pro
20

400

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

AAAATGTCCT CCACAGCTTT GCCCAGTGGG ACACATGGCT CCTGACATAC GTAACCCAGG    60
ATGGGATGCC TTGTTGAGT CTCTCAGATA TGGAGCAAAA TGGGCCATGT GCAGTCAAGA    120
CGCCATCTAM CCTGGGCAGC TTGCCTAAGC CTCGAGGGAC CTGCCA ATG ATG GAT      175
                                   Met Met Asp
CTG AGA CCT CTT CTG TCC CTG GCT GCC TAT CTG TCT GGT CCT CAT CAA      223
Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly Pro His Gln
-15                               -10                               -5
GAA CCC AGT GTT CCC ACC CGA GAT GGA GAC GTG AAT AAT CTT CCT AAG      271
Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn Leu Pro Lys
1                               5                               10                               15
CCT AAT CCT GCC AGA AGC GTG AAG CAA GGG GGA ATH TGG AAG GCG GAA      319
Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp Lys Ala Glu
20                               25                               30
CAG GAA AGA GTG GAA GTG GAG                                          340
Gln Glu Arg Val Glu Val Glu
35

```

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 147..203
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq LLPGLPLVRTSFS/HF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

```
AGCGGTCAGA GGATGCCCTC TTCGCCCTGT GAGCAGCTCT GTGGTTTGCC TCCCCAGATG   60
GCGGGTCCCC GCTTGCACCC CGTGGACACC GGGCACTGGC CACTCCTACA TCCCCAGCTC  120
CACACGGCCT GCACACCTGT GTTTCC ATG GAA ATG CCA CCG TGT CTG CTC CCA   173
                               Met Glu Met Pro Pro Cys Leu Leu Pro
                               -15
GGC CTC CCA CTA GTC AGG ACC AGC TTC AGC CAC TTC TTT TCT CTG AGT   221
Gly Leu Pro Leu Val Arg Thr Ser Phe Ser His Phe Phe Ser Leu Ser
-10                      -5                      1                      5
GGT GGG ACA ACT ACA GCC AGA GGG                                     245
Gly Gly Thr Thr Thr Ala Arg Gly
                               10
```

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 19..93
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq GLAMLHVTRGVXG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

| | |
|---|-----|
| ACATGCGCAG GAGGCTCA ATG ACA GTC GAG CTT TGG CTA AGG CTC CGG GGA | 51 |
| Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly | |
| -25 -20 -15 | |
| AAG GGT CTA GCC ATG CTG CAT GTG ACC CGG GGG GTC TRG GGG TCC AGG | 99 |
| Lys Gly Leu Ala Met Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg | |
| -10 -5 1 | |
| GTC CGA GTA TRG YCA MTG TTG CCC GCG CTC CTC GGG MCC CCC MGG GCC | 147 |
| Val Arg Val Xaa Xaa Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala | |
| 5 10 15 | |
| CTC TCA TCG MTG GCA GCC AAA ATG GGG GAK TAT CGC AAS ATG TGG | 192 |
| Leu Ser Ser Xaa Ala Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp | |
| 20 25 30 | |

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 7..78
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq LLILLCSSPPDRV/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

| | |
|---|-----|
| ACAAAC ATG TCT ATA GAA GAT TTT GTG AAT AGA AGC ATA CTT CTG ATC | 48 |
| Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile | |
| -20 -15 | |
| TTG CTC TGT TCT TCC CCA CCT GAT AGG GTC AGC TAC AGA GCC AAG GTT | 96 |
| Leu Leu Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val | |
| -10 -5 1 5 | |
| TTA CAC TCA TTG CTT CAA TTG CCC GCC CAG | 126 |
| Leu His Ser Leu Leu Gln Leu Pro Ala Gln | |
| 10 15 | |

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 32..91
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq FALLFLFLVPVPG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```

AAGTCTCAGC GTGGGGTGAA GCCTAGCAGC T ATG AGG ATC CAT TAT CTT CTG      52
                               Met Arg Ile His Tyr Leu Leu
                               -20                               -15

TTT GCT TTG CTC TTC CTG TTT TTG GTG CCT GTT CCA GGT CAT GGA GGA      100
Phe Ala Leu Leu Phe Leu Phe Leu Val Pro Val Pro Gly His Gly Gly
                               -10                               -5                               1

ATC ATA AAC ACA TTA CAG AAA TAT TAW TTG CAG AGT CAG AGG CGG CCG      148
Ile Ile Asn Thr Leu Gln Lys Tyr Xaa Leu Gln Ser Gln Arg Arg Pro
                               5                               10                               15

GTG TGC TGT GCT CAG CTG CCT TCC AAA GGA GAA AGG                        184
Val Cys Cys Ala Gln Leu Pro Ser Lys Gly Glu Arg
20                               25                               30

```

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 217..255
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.4
seq MCLLTALVTQVIS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

AATGCCAGTG TCAGCTTCTC TCCGAAACT GGGTAATACG AAATGGTCTT TATTGTTGT 60
GAACACTCGA GCTGAGAAAC ATTTTAGGAT CTTTGTGTCT TTTGTGATGA TTTTGTTCCT 120
GRAAGRWGGA AASCTGTCTA AAAATATTCA AGTGTGCAAC CAAGGATTTA GATGAAGCCA 180
GCAAACAAAG GAATCATGTA ATCAGGACCT GAGCGA ATG TGC TTA CTC ACG GCG 234
                               Met Cys Leu Leu Thr Ala
                               -10

TTA GTT ACA CAG GTG ATT TCC TTA AGA AAA AAT GCA GAG AGA ACT TGT 282
Leu Val Thr Gln Val Ile Ser Leu Arg Lys Asn Ala Glu Arg Thr Cys
      -5              1              5

TTA TGC AAG AGG AGA TGG CCC TGG NGC CCC TCG CCC CGG ATC TAC TGC 330
Leu Cys Lys Arg Arg Trp Pro Trp Xaa Pro Ser Pro Arg Ile Tyr Cys
  10              15              20              25

TCA TCC ACC CCA TGC GAT TCC AAA TTC CCC ACC GTC TAC TCC AGT 375
Ser Ser Thr Pro Cys Asp Ser Lys Phe Pro Thr Val Tyr Ser Ser
      30              35              40

```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 76..129
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq GLALVASTPPSR/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

ATCTGGCGCG TGGTCTTGCA TTTCTACTT GGTCTGTTC GTGGCGCCGC GCCTCCGGGT 60
GTTGGGGAGT CCGGG ATG ATG GGG AAT CCG GGG CTC GCC CTA GTC GCG GGG 111
      Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly
      -15              -10

ACA CCG CCT TCC AGG AGC TGT CCC CAG GCA AAC TCA CAG ACG CGG 156
Thr Pro Pro Ser Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg
  -5              1              5

```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 186..299
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq PCVSLWAPRXFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

ATAACCCATA TAGTAGTTAA GCCATTGTGG TGAGGGTGTT TGAAACCCAG CTATCCTATG   60
TAATGCTATT TCCAGGGGAA AAATATTCCC AATCCAGGT AAAAGATCAG AAACAGATAT  120
CACCTGSAWT TTGTTCCACC TTCACCCCAG GCTTCAGCTA TACTTAGGTA TTACTCTCTG  180
GTCCC ATG AAC CAT CTC ATG CCT TTG ACT GTG CTG CAC TCA GTG CTT GAA   230
  Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu
        -35                -30                -25

ATG CTC CGC ACA CCC CGC ACA CCT CCC TGG CCC TGT GTA TCC CTT CTA   278
Met Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu
        -20                -15                -10

TGG GCG CCC AGA GSA TTT GCT TCC TCT TGC TCT CAA GCA TTT ACC ACT   326
Trp Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr
        -5                  1                  5

CTG CAN KGC AAT TGC TTG CTT ACT AAT CCA TCT CCC ACA CTA GAT TGT   374
Leu Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys
   10                15                20                25

GAC CTC CCT GAG GGC TCA GAA ATA TTA AAT TCT TCT CTG TAT CCT CAT   422
Asp Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His
        30                35                40

TGC CTA CTC AGT GCT TGG AAC ACA CGA CAC TCA ACA   458
Cys Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr
        45                50

```

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 13..84
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SLLXLRASQLSEG/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```
ATTATTATTT TT ATG GGA CAT GTT GTG TTT GGG GAT ATA AAA AAT AGT TTA    51
      Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu
                        -20                      -15

TTA KGT TTA AGG GCT TCG CAG CTT AGT GAG GGA GAC ACA TGR VTG AAM    99
Leu Xaa Leu Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa
-10                      -5                      1                      5

TVA TGT CCA BRT ATG RTG AGA GGT AAA CAC ATA TCC TAT    138
Xaa Cys Pro Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr
      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 48..290
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq FLSLLXSVSETPG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```
ACTTCTTCCC CGGGTCTCCG AAGCCGCTAG GGAAGCGCAA GGGGCC ATG GCT GGC    56
      Met Ala Gly
```

-80

```

GGG AGG CGG GAT TAC AGC CAG CTC TTT GGC CGC GGC CCC GGT CGG CTC   104
Gly Arg Arg Asp Tyr Ser Gln Leu Phe Gly Arg Gly Pro Gly Arg Leu
      -75                      -70                      -65

TCG CGA GCG CGA GCC TCT GTT GTG CGT TGG TCT CCC CGG GCA ACT GCT   152
Ser Arg Ala Arg Ala Ser Val Val Arg Trp Ser Pro Arg Ala Thr Ala
      -60                      -55                      -50

TGC CCT GCG CCA CCG AGC CTC CCG GAT TTA AAG CGG CAG GAG CTG GTT   200
Cys Pro Ala Pro Pro Ser Leu Pro Asp Leu Lys Arg Gln Glu Leu Val
      -45                      -40                      -35

AGC CGG ATA GAA TGT GGG TGC CGA GGG CCG GTG GGG GCC ACC GCA GAC   248
Ser Arg Ile Glu Cys Gly Cys Arg Gly Pro Val Gly Ala Thr Ala Asp
      -30                      -25                      -20                      -15

TTC TTT CTG TCC CTG CTC TDC AGC GTC TCT GAA ACC CCT GGC AGC CTG   296
Phe Phe Leu Ser Leu Leu Xaa Ser Val Ser Glu Thr Pro Gly Ser Leu
      -10                      -5                      1

CGG RGA AAC GAT CTT TTC TTC GTC TCT CAG CTT ATT TGG GGC CGG   341
Arg Xaa Asn Asp Leu Phe Phe Val Ser Gln Leu Ile Trp Gly Arg
      5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 207..263
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LWCFFHFISFSL/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ATCCTCCATA GCTATATCCA TTTCCTGGGA CATGGGTTGG CCCAAGAGGG AATGAGAAGG   60
ACCTGCGATT GCACAGGAAA TTCTGGGGCA CATTTAACGT TAAATCATTA AGCTTCTGCC   120
AATAAATCCA TTACTGTTAA TTAACTGAG ATGGCCAACG ATCTGCTGAC AATATTCCTT   180
CATTGATTTT CATTCTCAGT GAATCG ATG TTC TGG CNT GGC TCT CTT TGG TGT   233
      Met Phe Trp Xaa Gly Ser Leu Trp Cys

```

-15

TTT CAT TCT TTC ATT TCT TTC TCC CTG TCC TCA TCA CGG 272
 Phe His Ser Phe Ile Ser Phe Ser Leu Ser Ser Ser Arg
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 118..225
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq FLLTFFSYSLHA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AGGCNNNCGG ASCSGGGCTG GAGAGCGGCS NCCACTGCGG ATCTCGGAAG GAAGAAATGA 60
 GTAAATCAC TCATSSAVAC TTAAAGGTCTN NNGTGAGAM GGAAGGTCAG GMAGAAC 117
 ATG GCC TGG CCA AAT GTT TTT CAA ABA GGG TCT CTG CTG TCC CAG TTC 165
 Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe
 -35 -30 -25
 AKN BAT CAT CAT GTT GTA GTG TTC CTG CTC ACT TTC TTC AGT TAT TCG 213
 Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser
 -20 -15 -10 -5
 TTG CTC CAT GCT TCA CGA AAA ACA TTT RGC AAT GTC AAA GTC AGT ATC 261
 Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile
 1 5 10
 TCT GAG CAG TGG ACC CCA AGT GCT TTT AAC ACG TCA GTT GAG CTG CCT 309
 Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro
 15 20 25
 GTG GAG ATC TGG AGC AGC RAC CAT TTG TTC CCC AGT GCA GAG 351
 Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 380..436
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq WILAVGLSLPSSS/XI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

ACTCTCTTCT ACTGGAATGG TACCCTTGTT GACTGACTCA TGTATAGCTG CTTGGCTTAA   60
TGGTAGACCA GATATTCAGG TCCTCTGAGA CAGGCCCTG ATGACTTTTG CAACTACATC  120
TTTCAMCACA GCCTGCCTTG CATTTTGGAC TCTAGCAACA CTGAAATACA TGTCATTTCC  180
CAAGGCATGT TAAGCTGTTT CTATTCTCTA GGCTCTCCCT TTTTCCTAGA ATGCCCTTTT  240
CCTCTAGGCT AATGTCTTTC TCCTTTAAAT TAGTCATCTT CAACAAAGGC TACCTTGACC  300
TTCTCTTGAC TTTGCCACAT TCCTGCTGCT GCCTTCCTTC CATGGCCTTT GTCACGCTAT  360
ATGGTAATTG ACAGGTTCC ATG ATC TTG AGG AAC TTA TGG ATT TTA GCA GTG   412
              Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val
              -15                               -10

GGT CTT AGC TTG CCA TCT TCT TCA MCC ATC AAG TTT CAT TTC TCT CTT   460
Gly Leu Ser Leu Pro Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu
      -5                               1                               5

TAC TCA                               466
Tyr Ser
      10

```

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 267..371
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq LCGLLHLWLKVS/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

ACAATCAGTT TGCCAATACC TCAGAAACAA ATACCTCGGA CAAATCTTTC TCTAAAGACC   60
CTAGTCAGAT ACTAGTCAAT ATCAAATCAT GTAGATGGCG GCATTTTAGG CCTCGGACAC   120
CATCCCTACA TGACAGTGAC AATGATGAAC TCTCCTGTAG AAAATTATAT AGGAGTATAA   180
ACCGAACAGG AACAGCACAA CCTGGGACCC AGACATGCAG TACCTCTACG CAAAGTAAAA   240
GTAGCAGTGG TTCAGCACAC TTTGGT  ATG TTG ACT GTT AAT GAT GTA CGT TTC   293
                               Met Leu Thr Val Asn Asp Val Arg Phe
                               -35                               -30

TAT AGA AAT GTC AGG TCC AAC CAT TTC CCA TTT GTT CGA CTA TGT GGT   341
Tyr Arg Asn Val Arg Ser Asn His Phe Pro Phe Val Arg Leu Cys Gly
-25                               -20                               -15

CTG TTA CAT TTA TGG CTT AAA GTC TTT TCT CTT AAA CAG TTA AAA AAA   389
Leu Leu His Leu Trp Leu Lys Val Phe Ser Leu Lys Gln Leu Lys Lys
-10                               -5                               1                               5

```

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 111..179
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.9
seq LFLNL...LAXPFS/KQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

ATTAATTTTA ATTTTCATTG TCAATATTTT GAGCTTAGAA CATTTATGGT ATAAAAATTT   60

```

```

AAACTAATCA AAGTTGTGTG ATGATTCCG GGAATTATTA TTGAAAGCCT ATG AAT      116
                                   Met Asn

TTA AAA CCA GGT TTA CCA TGT AAT TTG TTT TTA AAT TTA TGT ATA CTA      164
Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys Ile Leu
  -20          -15          -10

GCC TGV CCT TTC TCC AAG CAA ATT ATT GAA CTA TTA GAA TAT GTT AGT      212
Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr Val Ser
  -5              1              50              10

TAT CAT CCT TGT GTC TTA GTA TAT AGT GAA TAC AGM AAC ATC AGC ATT      260
Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile Ser Ile
          15              20              25

GTA TAC ACT CTT      272
Val Tyr Thr Leu
          30

```

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 43..162
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq VVLAWGLLNVSMA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

ACCAGAGAGA GTGGCGCGAG CTGCGTTTTC CGGCCAGAGG AC ATG ATG CAG GGG      54
                                   Met Met Gln Gly
                                   -40

GAG GCA CAC CCT AGT GCT TCC CTT ATT GAC AGA ACC ATC AAG ATG AGA      102
Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg
  -35          -30          -25

AAA GAA ACA GAG GCT AGG AAA GTG GTC TTA GCC TGG GGA CTC CTA AAT      150
Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn
  -20          -15          -10          -5

GTA TCT ATG GCT GGA ATG ATA TAT ACT GAA ATG ACT GGA AAA TTG ATT      198
Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile

```

| | 1 | 5 | 10 | |
|---|----|----|----|-----|
| AGT TCA TAC TAC AAT GTG ACA TAC TGG CCC CTC TGG TAT ADY GAG CTT | | | | 246 |
| Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp Tyr Xaa Glu Leu | | | | |
| | 15 | 20 | 25 | |
| GCC CTT GCA TCT CTC TTC AGC CTT AAT GCC TTA TTT GAT TTT TGG AGA | | | | 294 |
| Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg | | | | |
| | 30 | 35 | 40 | |
| TAT TTC AAA TAT ACT GTG GCA CCA ACA AGT CTG GTT GTT AGT CCT GGA | | | | 342 |
| Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly | | | | |
| | 45 | 50 | 55 | 60 |
| CGG | | | | 345 |
| Arg | | | | |

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 274..330
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq PXXLLILAHITQS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

| | |
|--|-----|
| AGTATTGTGTT AAATGCTACA AGAGTGACTG GGATCATAAG TGTTACGGGA GTTTGGCAAA | 60 |
| GAAGCAGGAG GTAGTTAGTG TAACTGTTAA TGTGATTATA AGACTAATAC ATTTTGTKGG | 120 |
| RAGATAACTT ACCAAGTTTG GTTTGTGGAA AATTGGATT GAGAAGGAAA TTGTATGTTT | 180 |
| CCGTTAGAAG TAGAACAACA ACAACAAAAT ATCTCCCATC ATTGTTTGG TACTATCTGG | 240 |
| CCTCCCCAGT GCTGCTTGGG AGAATCATGA AAC ATG ATG AAT CAA ACA CAT CCT | 294 |
| Met Met Asn Gln Thr His Pro | |
| -15 | |
| TRM RTG TTG CTC ATC CTG GCA CAT ATT ACA CAG AGT TGC CCA TGG GCC | 342 |
| Xaa Xaa Leu Leu Ile Leu Ala His Ile Thr Gln Ser Cys Pro Trp Ala | |
| -10 -5 1 | |
| CAT GTA GGA GCA GCT CCA TCT GCC CTT CTA ATA CAT AGG TGG GAR CTG | 390 |

His Val Gly Ala Ala Pro Ser Ala Leu Leu Ile His Arg Trp Glu Leu
 5 10 15 20
 AGG GGG TGC TCG TAT TTG AAA CTG TTT TTG GTT ATG GTG CTC ATA TTT 438
 Arg Gly Cys Ser Tyr Leu Lys Leu Phe Leu Val Met Val Leu Ile Phe
 25 30 35
 GAA ATG CTT 447
 Glu Met Leu

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 35..94
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq GLVLLLSLAEILF/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

AGTCCTACTC AGAGTTTCT GTGAAGGCAA GGGC ATG GGG TTG CCG GAG AGA AGA 55
 Met Gly Leu Pro Glu Arg Arg
 -20 -15
 GGA TTG GTC CTG CTT TTA AGC CTA GCT GAA ATT CTT TTC AAG ATC ATG 103
 Gly Leu Val Leu Leu Leu Ser Leu Ala Glu Ile Leu Phe Lys Ile Met
 -10 -5 1
 ATT CTG GAA GGA GGT GGT GTA ATG AAT CTC AAC CCC GGC AAC AAC CTC 151
 Ile Leu Glu Gly Gly Gly Val Met Asn Leu Asn Pro Gly Asn Asn Leu
 5 10 15
 CTT CAC CAG CCG CCA GCC TGG ACA GAC AGC TAC TCC ACG TGC AAT GTT 199
 Leu His Gln Pro Pro Ala Trp Thr Asp Ser Tyr Ser Thr Cys Asn Val
 20 25 30 35
 TCC AGT GGG TTT TTT GGA GGC CAG TGG CAT GAA ATT CAT CCT CAG TAC 247
 Ser Ser Gly Phe Phe Gly Gly Gln Trp His Glu Ile His Pro Gln Tyr
 40 45 50
 TGG ACC AAG TAC CAG GTG TGG GAG TGG CTC CAG CAC CTC CTG GAC ACC 295
 Trp Thr Lys Tyr Gln Val Trp Glu Trp Leu Gln His Leu Leu Asp Thr
 55 60 65

AAC CAG CTG GAT GCC AAT TGT ATC CCT TTC CAA GAG TTC GAC ATC AAC 343
 Asn Gln Leu Asp Ala Asn Cys Ile Pro Phe Gln Glu Phe Asp Ile Asn
 70 75 80

GGC GAG CAM CGG 355
 Gly Glu Xaa Arg
 85

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 305..388
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LCWALLYNCFSSS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

ATCAGTCTGT GGAGACAGGT GAGCACGAAC TTCTGAGACA GGCTGGGTG CGAGGGTCGG 60
 GAGGGTCATG GGATTGGGAC CGAGGTGTGA GGAGGGAATC TGCAATTCCT TGCTACACAG 120
 AGCGCTGGCA ACTTCTGACA GGCTGTTTCT GGGGTATGGG CTGCCTCGGG TTGTTGCTGT 180
 TACAAGGAAA GAAAAGAGTT CCCCTGCCCA CCGCCTCCCA GCCACTGGGC TACCTCCTGG 240
 CAGGAAATTT GCAAACCTGAG TTTAACAAGT TAGGATCAGC AGAGGGTAGA GGAGGGCCTG 300
 GCAG ATG TGG GGT CTA GAA GAG GAC AGG AGT TAT CAG GGS CTC CGG CCA 349
 Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro
 -25 -20 -15
 TTG TGC TGG GCT TTG CTG TAC AAT TGT TTC TCA AGC AGT TGT GTY CCT 397
 Leu Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro
 -10 -5 1
 GTG GCT TTG GTG 409
 Val Ala Leu Val
 5

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 129..383
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ALLASLGIAFSRS/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

AGTAGCGGAC ATTTTGTTC TGTCAGGCTG TCCCTGGCCG GGGTTCTGTA ACGCTTGTT 60
GGGCCGCAGG TGGAGGTGTT GGGAAAGCGC GGAGGAGATG TTGTCCCAG TGTCCCAGAGA 120
CGCGTCTG ATG CTC TGC AGG GAC GGA AGT GCC TGC GTC CCC CGA TCG AGA 170
    Met Leu Cys Arg Asp Gly Ser Ala Cys Val Pro Arg Ser Arg
    -85                -80                -75

CGC CTG CCG CTC CCG GCA GCT GTC CGC GCC CAC GGT CCT ATG GCG GAC 218
Arg Leu Pro Leu Pro Ala Ala Val Arg Ala His Gly Pro Met Ala Asp
    -70                -65                -60

TGN NCG GAC TCC GCG CGG GGC TGT GTG GTC TTT GAG GAT GTG TTT GTA 266
Xaa Xaa Asp Ser Ala Arg Gly Cys Val Val Phe Glu Asp Val Phe Val
    -55                -50                -45                -40

TAC TTC TCT CGG GAA GAA TGG GAG CTT CTT GAT GAT GCT CAG AGA CTT 314
Tyr Phe Ser Arg Glu Glu Trp Glu Leu Leu Asp Asn Ala Gln Arg Leu
    -35                -30                -25

TTG TAC CAT GAT GTG ATG CTG GAG AAC TTT GCA CTT TTA GCC TCA CTG 362
Leu Tyr His Asp Val Met Leu Glu Asn Phe Ala Leu Leu Ala Ser Leu
    -20                -15                -10

GGA ATT GCA TTT TCC AGA TCA CGT GCA GTC ATG AAA CTA 401
Gly Ile Ala Phe Ser Arg Ser Arg Ala Val Met Lys Leu
    -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 61..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq FLCFLNLTSHLSG/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

ATACCTAATG ATAACACAGT ATCTCTTCGA ATTTGTACTA TTGCAGAACA TTTAGAAACA    60
ATG CTT ATT ACT CGK TTA CAG TCT GGT ATA GAT TTT GCA ATC CAG CTT    108
Met Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
-55 -50 -45

GAT GAA AGC ACT GAT ATT GGA AGC TGC ACA ACA CTT TTA GTT TAT GTC    156
Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
-40 -35 -30 -25

AGA TAT GCG TGG CAA GAT GAT TTT TTG GAG GAT TTT TTG TGT TTT TTA    204
Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
-20 -15 -10

AAT TTA ACC TCA CAC CTA AGT GGA TTA GAT ATT TTT ACA GAA TTA GAA    252
Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
-5 1 5

AGG CGC GGG
Arg Arg Gly
10
261

```

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 191..304
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7

seq LAFLSCLAFLVLD/TQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

AACTCTGCAG GGCCTCCAAG GCCAGGCTTC AGGGCTGGGA CTCAGTCCTG AGGCACTGGG    60
GAGCCATGAG GGGCTGTGGC AGGGAGGGGC AGGGTGTGGA AAGACTCCCC TGGGGCCATG    120
GTGGAGATGT GCTGAGGTCT TCTCCCTGAT CGTCTTCTCC TCCCTGCTGA CCGACGGCTA    180
CCAGAACKAG ATG GAG TCT CCG CAG CTC CAC TGC ATT CTC AAC AGC AAC    229
           Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn
           -35                               -30
AGC GTG GCC TGC AGC TTT GCC GTG GGA GCC GGC TTC CTG GCC TTC CTC    277
Ser Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu
-25                               -20                               -15                               -10
AGC TGC CTG GCC TTC CTC GTC CTG GAC ACA CAG GAG ACC CGC ATT GCC    325
Ser Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala
           -5                               1                               5
GGC ACC CGC TTC AAG ACA GCC TTC CAG CTC CTG GAC HKC ATC CTG GCT    373
Gly Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala
           10                               15                               20
GTT CTC TGG
Val Leu Trp
           25

```

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 190..273
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq DHLFLLFPRSCSS/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

CTCTTGTTAA CCTGTCTTTT GCTATAGGAG TGTCAGACCC TTATGAGGGG AGAGGAGAGA    60
TATCATACTT TTTCTACCTC TACACTTTTA ATATCATTAA TTTTCTAACA ATGCCCAAT    120

```

CTTCAGTACA CCTCTCTCTC CTGAACCCCTA TACTTGTACA GCAACTTTCT ATGTGACATT 180
 TCTTCTTAA ATG TCT AAT AAG TAT ATC AAA CCT AGC ATG TCC CCA GGA AAC 231
 Met Ser Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn
 -25 -20 -15
 ACT GAT CAT CTT TTC CTA CTC TTC CCC CGA AGT TGT TCC TCC CTC GTC 279
 Thr Asp His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 263..334
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq FFFFLFLLPPXPP/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

ATATGTGTAA TGTCTTTATT CCTTAGACTA TGGTCTCCGT GGAAGATTAC TGATACTCCC 60
 ACTAGTATTA ATAACAATGT TAGGTAACAT TACTGAATGT TTACTGAGTG CCAGGTAATG 120
 TTCTAATTGC TTTACATGTA TTAGGCTATG TATTCCTCAC ATGAACCATA TGAAAGAGAT 180
 ACTCTTATTG TTGTCATTTT AGAAGTGAAG AACTGAGGC ACAGAAACT TAAGTAATTA 240
 GTCCAATTCA TACAGGTAGT AT ATG GTA GAA CTG AAG CAG TTG GGC CCC AGG 292
 Met Val Glu Leu Lys Gln Leu Gly Pro Arg
 -20 -15
 TCT TTT TTT TTC TTT CTT TTT CTT CTG CCG CCG RET CCT CCA ACC GGG 340
 Ser Phe Phe Phe Phe Leu Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 17..94

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LILPALFFFPLHC/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

AARACCTTC TCAGTG ATG CCT TAC GTC ACC ATC CCA TAT ATA ATA GTG TAC    52
      Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr
      -25                      -20                      -15

TCA CTC ATT CTA CCT GCC CTC TTT TTT TTC CCT CTC CAC TGT ACT TTT    100
Ser Leu Ile Leu Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe
      -10                      -5                      1

CAC GGT CTA ACA TAC TAT ATA TCA TGT GTT TGT TCA TTA TCT CTA CCC    148
His Gly Leu Thr Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro
      5                      10                      15

ACG
Thr
151

```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 247..321

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq LLLCMDLPHSVLS/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

AATTATTCTA TAAACTTCT GGCTGGATTT AATACTAGG CAGTATTCCA AGGGATGATA    60

```

```

AAATGTTTTT ACAAACCTAA TTAGACCCAT TTTTGTAATT AACTTTTATT ATACATGTGC 120
TATGAGGATT AACTTTTGCC TCATAAAAGT ATTCTGACAG GTGCTTTGCA CAGAGTAAAGT 180
CCGCCAAAGT GGACGTTCTC ATATGTAATT CTGAGCTTAC TCATACTGCC CAGGAAGGAC 240
GTGCAC ATG CCA CCT TTG GCA GCT GTG ATG GGG AGC CTG CCT CTG CTC 288
      Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu
      -25                -20                -15

TTG TGC ATG GAC CTT CCA CAT TCT GTC CTG TCC AAC TGG 327
Leu Cys Met Asp Leu Pro His Ser Val Leu Ser Asn Trp
      -10                -5

```

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 186..248
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq EFLEFLGFPSNSWP/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

ACAGCTAGAA TATGTTGGAT TCAGGAGCTT GTCCATTATT TGTAGGTAAA AAAAGCTGCA 60
CGTAGATTTG ACTTCAACTC CGTAAAAAAG ACAGCTGTAT TTTCCGTCCA ACTGGAATTG 120
TTGAATCACA CTGCATAGCT GCCCAAAGA GAGTGTGTTGG TCTTGAACCT TCTATACTTT 180
TATAA ATG TTA CAA ATT CCC GAA AGA AGG GAA TTT TTT TTT CTG GGG TTT 230
      Met Leu Gln Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe
      -20                -15                -10

CCT TCA AAC TCT TGG CCC CAC AGG 254
Pro Ser Asn Ser Trp Pro His Arg
      -5                1

```

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..102
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq FLITLFCCCVVVG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

ACATGSTATCT GTTGGCTATT TGTATATCAT CTTTGCATCT TTGGATAA ATG TTC TTT      57
                                     Met Phe Phe

GTC CAT TTT TTA ATC ACT TTA TTT TGT TGT TGT GTT GTA GTG GGG TTT      105
Val His Phe Leu Ile Thr Leu Phe Cys Cys Val Val Val Gly Phe
-15                -10                -5                1

TTT GGC CAT GAT CAT TCA TTT ATC TCA CAG TTC ATT CTT GTT ACT TGG      153
Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu Val Thr Trp
          5                10                15

GCC AGG GCA GGG                                165
Ala Arg Ala Gly
          20

```

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..157
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq CLLHLRCLQLYWA/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

ATCAGTGTAT TTTTTTATA GATTTAAAAT ATACCTGAAA ACTTTTCTAG GAAGAATAAT 60
 TATTCATGGA AAGAGCATTG TA ATG GCA TGT TTT GGG GAG AAA AGA CAT GCC 112
 Met Ala Cys Phe Gly Glu Lys Arg His Ala
 -25 -20
 AAG TCT TGT TTA CTA CAT TTA AGA TGT TTA CAA CTA TAC TGG GCT GCT 160
 Lys Ser Cys Leu Leu His Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala
 -15 -10 -5 1
 CGG 163
 Arg

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 279..362
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq PLSLALQSSCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

AATAAACCTT ACTTTAACAG AATTAAACAG ATATCTCTTT AAAAAACTGC TTTAATGTTT 60
 TTACCTTCTA TCTTCTTTTT CTCCAGCTTT ATCCTGACAG RGAAGTTAGC ACTAATTAAT 120
 CTATTTTCTC TTCCCCCTCT TTTTCCCTT GTGTGTGTCT TTTCTGCCTT CATCTACCCC 180
 AGTGAATTG TTCAGCATTT TGGCTCACTC ATTTCTTCAG CTAACCTACAG CTTACTACTA 240
 CAGCCACCAC TACTAGAGCC ACTCCTGTCT CATCCTGG ATG GTT GAC AGA GAT GAA 296
 Met Val Asp Arg Asp Glu
 -25
 AAC ATC TTG CTA AAG CAA ATA TAC AGY CCC CTT TCA CTG GCT CTC CAG 344
 Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro Leu Ser Leu Ala Leu Gln
 -20 -15 -10
 FCC TCC TGC TGT CTT TGC TTG ACC TCC TGC 374
 Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys
 -5 1

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 115..174
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

ATAAATTTA CAGAAAAGTT GCAAAGAAGA TAGAATTTCT GCCTAGCTTT TGCCCCAATT      60
TCCCAC TTGC CACCCTTCCC TCTTTGTGTT TGTATCTTTT TTTTCTGAG CCAC ATG      117
                                         Met
                                         -20

AAA GTA AAG CCG CCT TTT GTG TCT GTG TCA CTC TGT GTG TGT GAC TGT      165
Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp Cys
          -15                      -10                      -5

GTA AGG GGT AGC ACA CTT ACA TGG AAC AGG TTA CTG CGT GTG GGA GGG      213
Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly Gly
          1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 63..184

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4

seq ILLTSCFYTLVSS/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ATGGCTAACA TATTCTTTTT TTTTCTCTG TAGTAGTTT TTGAAAGAAG AAATAGGCTA   60
TTCTAGC ATG ATC TCA TCC TGT GGA GTT AAA TAC TTG TTT TCA CAT GCC   109
      Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala
                        -35                      -30

TCC TTA TTT TTT ATG GTA GGG AGT ACA GGA AGT TTA ATA CTC TTA ACT   157
Ser Leu Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr
-25                      -20                      -15                      -10

TCT TGT TTC TAT ACC CTT GTT TCA TCA ACC TTT CTT GAA AAA CTC TCT   205
Ser Cys Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser
                        -5                      1                      5

TCT TTG CTC TTG ATA TTA TTT ACC GAA ACA AGT GGT CTT ATG TTA AAA   253
Ser Leu Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys
      10                      15                      20

ACA TTT GTA GCT AAT TCT TGC TGT WAA TTG TGG TCT CAC AAT TGT ATT   301
Thr Phe Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile
      25                      30                      35

AAT TTC TTC AAA AAG GTC CKG CCT TCT TAT TGC KGC AGC AGT CTA CTC   349
Asn Phe Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu
      40                      45                      50                      55

TTC CTG GCC GTA CCT AGG
Phe Leu Ala Val Pro Arg
                        60

```

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 174..233

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4

seq SFLCNFLVSLSL/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:


```

AGAAGGGGGT GAAAGGAGTA ACTGCTATAT TTAGAAGGAG GTTAAGGATA GCAATTGATT   60
TTAAGGGTGG GGCTAGGGAA CTTGTCTTTA AAATCCTGCA TTGCACAGC AAGCACAGTT  120
CGTATTGAGA TTTTGCTATT TGGAAGTGTG AGGGAGGTAT AGGATGCTGC CTA ATG      176
                                         Met
                                         -20
GGA GGT GGG ATH GCA GAG AGT TTT CTA TGT AAT TTT TTG GTA TCA CTT      224
Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser Leu
          -15                -10                -5
TCC CTC TCT TTC CTC CAT GGC CGG
Ser Leu Ser Phe Leu His Gly Arg
          1                5

```

248

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 265..363
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq LAYFLCCQGVIFG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

CTATTTCTCA TTGTCTGTCT GGTTTTCCAT CCCCCTCACA TGTGGTGACC AGCACCTGGC   60
CCGCCACGGC ASCCAGGAGG CATTGTGTTAA GCGAATAATC GAGACAGGGA AGAGGAGTGG  120
AGTTGGCTGC TCCAGACTCT GCTTAGTTTT CCTTCTCAA AGTTCTCCCT CCTGTGTCCT  180
AGCCGGGGAA TTAGCTAAAA TGGAATTTTC TTTGGTGATC AGGTATCCTT CTGATGAAGA  240
GAAGAAAGGC CTAAACTCCC AGGC ATG GAT GCA TTA GAA AGA GGT AGT CTT      291
          Met Asp Ala Leu Glu Arg Gly Ser Leu
          -30                -25
AGA AAT GAG CAG GCG TTG GTT ATT TAT GCA GGA CTS GCA TAC TTT CTS      339
Arg Asn Glu Gln Ala Leu Val Ile Tyr Ala Gly Leu Ala Tyr Phe Leu
          -20                -15                -10

```

TGC TGC CAA GGG GTG ATT TTT GGA AGT CTC CCC TCT AAT GCT GGT GCT 387
Cys Cys Gln Gly Val Ile Phe Gly Ser Leu Pro Ser Asn Ala Gly Ala
 -5 .1 5

GGG CCT TTG GGA TGG TCT AGC
Gly Pro Leu Gly Trp Ser Ser 408
 10 15

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 79..194
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq SLWFLPLPTHTVYT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114;

| | | | | | | |
|---------------------|---------------------|-----------------|--------------|------------|------------|-----|
| TTGCTTGAAC CTA | CTGTCT TGT | TTTTTGT | C TTCCTGTGAG | TTCAAGGACA | GGAGCAGTGC | 60 |
| TTAACACACA GTAGGTA | ATG GAA TAT TTG | TTC CAG CAG CCT | GGA CAC TCA | 110 | | |
| | Met Glu Tyr Leu Phe | Gln Gln Pro Gly | His Ser | | | |
| | | -35 | -30 | | | |
| AGG GGA GAA GCC AGG | GCT GCT GCT GCC | TCT CTG GAA ACC | CTG TCT TCC | 158 | | |
| Arg Gly Glu Ala Arg | Ala Ala Ala Ala | Ser Leu Glu Thr | Leu Ser Ser | | | |
| | -25 | -20 | -15 | | | |
| CTT TGG TTT CTG CCT | CTC CCA ACC CAC | GTG TAC ACA CAT | ACA CAT GCC | 206 | | |
| Leu Trp Phe Leu Pro | Leu Pro Thr His | Val Tyr Thr His | Thr His Ala | | | |
| | -10 | -5 | 1 | | | |
| AAC | | | | | | |
| Asn | | | | | | 209 |
| 5 | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 283..327

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3
seq SSMLITILSFIFA/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```
ACCACAGTCA CTGTCACATT ATTCTGTTTT GTATTTTATT TACAGCTCTT ATAATTATCC   60
GAAC TTACAA ATTTATTTTC TTGTGTTTTC TCCGCCTGCT CCTCCACTTC ATTCTGTAAT  120
ACTATAGTTC ACTATAATAC TTCTAGTTCC TAGGACTGGA ATTATGTGTC TGGCACATAG   180
TAGACAGTAG ATGTTCAATTG AATGAATGAA TGATTCAAAT GAGATTTAAA TAGCAACAGT  240
CCTGACAGAA TGGTAAATTT CCACACTTAA GATGGTCTGT TA ATG GTA TCA TCA   294
                               Met Val Ser Ser
                               -15

ATG TTG ATA ACT ATT CTA TCG TTT ATT TTT GCC TTA GGG TAC CAC ACA   342
Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu Gly Tyr His Thr
-10                               -5                               1                               5

GCT TCT TAT CCA GTC TCC CTT CAT CCA CTC TCC TTT TTC CTA CAC       387
Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe Phe Leu His
10                               15                               20
```

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 315..369

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3
seq MNLVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ACAGTACTTG GAGGTATTCT AAAGGCAGAC ATACTTTATC TGAGCAGGTG CTTTGGCGT    60
GGTCCTGCCA AGAAAGAAAC AATGGCTTAG ATGACGTCTA TTCTAAGGCC TCAAGGCTTG    120
CACCCCTGCC ATGCTAAATA CAGATGCGCT CCTCCACCAA GAGAATCCCC TCTGCCCTCT    180
GCCATCTCAG CCCCAGCCCA GCTCAGCTGC CCATGACCTG TGTGCAAAGC AGGGGGCGGG    240
ACAAACAGCT ATCGCCTTTG GCCTTCCCTT TGCTCCTGAC AGCGGTCTCA AACCTGGAGG    300
AGTCAAAGGT CCAAG ATG CCT TTG TTC ACT ATG AAC CTG GTG TCA GCT CTA    351
          Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu
          -15                               -10

GCG TCC TCA GCA RCA GGG CAG CGT GGA GCA GGG CCA GCC CTC TGG CAC    399
Ala Ser Ser Ala Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His
   -5              1              5              10

TTG TGT
Leu Cys
                                         405

```

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 110..226
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LILLHCSIRVFF/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

CTTGCTTGTA AACATAAGCA TGTATTATTA CCTAGGCTTT GAATTTCAAA ATACGGTGTA    60
AACTACTCAT GGTAATATAG ATCTTGTTAG ACAAACGTTT ATGTAAAAA ATG ATC TGC    118
          Met Ile Cys

AAG CAT TAC TGT ATA AAG AAA AAT AAC CTG GAT TAC TTG AAT AGA ATG    166
Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu Asn Arg Met
   -35              -30              -25

GTT TAC AGT GCT CAG TTA AAG TTG ATA CTT CTT CTA CAT TGC AGT ATT    214

```

Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu His Cys Ser Ile
 -20 -15 -10 -5

AGG GTT TTT TTT TTT TTT
 Arg Val Phe Phe Phe Phe

232

1

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 232..390
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq SFLLLQLIHEDKA/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AATTTGAGAA GTGCCCTCCT ATACTTAGAG AAAAGGAATA TCCATATCTC TGAAGACACA 60
 GGGACACAGA GAGAATCTGA ACACACAGCC TTGGTAGGAT TCCTTCCGTT TATCATCATT 120
 AGATCATAAC CCCYTTTGTC MAGTCCTATT TCTCCARGAC TGCCTCCTTC TTCATTAAAC 180
 CTTGCATAAA AACTCACAAA TTTAACCATT TATTGGATT CTTATTTCCT T ATG AAA 237
 Met Lys
 ATT CCT GTG TGG CAT AAA ACG TGC TTT TTA AAA TCT GAA AGT TTT TCT 285
 Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser Phe Ser
 -50 -45 -40
 CCT GAT AAT TTA TCT GTT AGT TTG CCT TGT AGA CCT AGC CAG GTA CCC 333
 Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln Val Pro
 -35 -30 -25 -20
 TCA CAG GGG CAA GGA AAA TCT TTT CTC CTC CTA CAA CTT ATA CAT GAG 381
 Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Leu Gln Leu Ile His Glu
 -15 -10 -5
 GAT AAA GCC ATC CAG AAT GAA GCT ATT TTC CAG CCT TCT CTG CAG CTG 429
 Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu Gln Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 133..189
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq FGCTFVAFXPATA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

AGTCTGGGGG TGACATTGCA CCGCGCCCCT CGTGGGGTCG CGTTGCCACC CCACGCGGAC   60
TCCCCAGCTG GCGCGCCCCT CCCATTGCC TGTCTGGTC AGGCCCCAC CCCCCTCCC   120
ACCTGACCAG CC ATG GGG GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG   171
          Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala
          -15                               -10

TTC DGC CCG GCC TTC GCG CTT TCH TTG ATC ACT GTG GCT GGG GAC CGT   219
Phe Xaa Pro Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg
   -5                1                5                10

GGG
Gly                                     222

```

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq LWSSCNLAPLADG/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

AAGATGAAGA GGAGGCDGTG GCAGTGGTGG AAGAAGAGGC GCGGCGGCGG GGGTAGGGAG      60
CCTGGAAACG CGAGCGGGG ATG GTA GGT GGT TTG GAC CCG CCG GGC CGC CGT      112
      Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg
                        -30                        -25
CGT TTC CAG AAA GGG TTT GAC TGG AGG AAC CTC TGG AGC AGC TGT TGG      160
Arg Phe Gln Lys Gly Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp
      -20                        -15                        -10
CTG GCT CCT CTG GCT GAT GGC ATG TTG AGG TAC ATG GGC CAG CVG CAG      208
Leu Ala Pro Leu Ala Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln
      -5                        1                        5
CGA NGG GCA TCC AAT CCA GAG GGG TCC ACT CTA GAG GCC AGG CCA CCA      256
Arg Xaa Ala Ser Asn Pro Glu Gly Ser Thr Leu Gln Ala Arg Pro Pro
      10                        15                        20                        25
GCA CCA TRG GCC AGT GTG TCA CCA AGT GTA AKH MTC CCT CAT CGA CCC      304
Ala Pro Xaa Ala Ser Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro
      30                        35                        40
TGG GCA GCA AAA ATG GAG ACC GTG AGC CCA GCA ACA AGT CRC ATA GCA      352
Trp Ala Ala Lys Met Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala
      45                        50                        55
GGC GGG
Gly Gly
      358

```

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 110..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SLLVVDIFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

| | |
|--|-----|
| ATAGAACTAC TCGGAACCT CAAAATCAGT AGATTGGAA GTGATTCAA GCTAACTTT | 60 |
| TTCTTGGCC CTCCKTGTGT TCTAATTGCT TTGCAAGTGT AAKACTAGG ATG TCC AAG | 118 |
| Met Ser Lys | |
| -20 | |
| ATG CCA GTT TTT GCT TCT TTG TTA GTT GTC AGC TGC TTT TAT CAA ATT | 166 |
| Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe Tyr Gln Ile | |
| -15 -10 -5 | |
| TCA GGC CGC TGG | 178 |
| Ser Gly Arg Trp | |

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 136..180
(C) IDENTIFICATION METHOD: Von Heljane matrix
(D) OTHER INFORMATION: score 5.1
seq VTQLLPFSPPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

AACAAAGAGA CACAGACAGG GGACTGTCAG CYGGYACCGG AGGMGCGGAC AACGAGTTAT      60
CAGCAACTSA AAGCACCTGA BGGGCCGCAC ATTCCANCCC CAGCCCAGTC CTCGTCCTCC      120
ACGCCAGCNC CAAGC ATG TSA GTA ACC CAA CTT CTC CTT TTC TCC TCC CCA      171
          Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro
          -15                      -10                      -5

GAC TCT GCG GGT CCT TTT CTG TCC CCT TTC TCT      204
Asp Ser Ala Gly Pro Phe Leu Ser Pro Phe Ser
          1                      5

```

(2) INFORMATION FOR SEQ ID NO: 123:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 1..102
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SFHFLPWALGAMA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

| | |
|---|-----|
| ATG GGG AAA GCA TGG CAA GAG ATG AGG GTG GAA TGG GGG GCA GAC AAG | 48 |
| Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys | |
| -30 -25 -20 | |
| GGG AAT GTC AGA AGC AGC TTC CAC TTT CTC CCC TGG GCA CTG GGA GCC | 96 |
| Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala | |
| -15 -10 -5 | |
| ATG GCA AGT TCA GAG CAG GGG AAG GAG AGG TCC AAC TTG TGC TTT AGG | 144 |
| Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg | |
| 1 5 10 | |
| AAG ACT CCT CTG GCT ATC ACG GGG AGA GGA ATT GCC AGG AGA CCA GGG | 192 |
| Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly | |
| 15 20 25 30 | |
| GGA GGT TGG ATG GGA ATG TGG GTG | 216 |
| Gly Gly Trp Met Gly Met Trp Val | |
| 35 | |

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 2..142
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq VIRLSQFLLKCWP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

A ATG AAA GTG ATG ATG AGG AAG AGG AAG AAA AAG GAC CAG TGT CTC CCA 49
 Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
 -45 -40 -35

GGA ATC TGC AGG AGT CTG AAG AGG AGG AAG TCC CCC AGG AGT CCT GGG 97
 Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
 -30 -25 -20

ATG AAG GTT ATT CGA CTC TCT CAA TTC CTC CTG AAA TGT TGG CCT CGT 145
 Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
 -15 -10 -5 1

ACA AGT CTT ACA GCA GCT ACG 166
 Thr Ser Leu Thr Ala Ala Thr
 5

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 254..361
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
 seq SFSIXTLLWGLNC/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ACTGTTTTAG TGTGTTGAAT ATCTTCTTCC AGAGTTTGAT GTATATGTAT CTTGGAGGTA 60

TATGTATTTT TAATTATATA AATATTTGAC CCTCTTTGCC TARTTTGTTT TATTCAC TTC 120

AACTTTGACC CTTTATACTT CTTTCTAAAT TTCACCTTCT TATGTTTGTT TTTCTACTTT 180

TCCTCAATGC CCTTTGTAAA ATTTTCATTT GAATCTATTA TTCTCCCTTG GACGTCTTAA 240

TTCTTCTCT ACT ATG ACT TTT TCT TTC TTT TGT TTC TTT CCT GGG TTC 289
 Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe
 -35 -30 -25

AGG CCA CTC CTG TTT CAT TAC TTT CTT TTT WNK TCC TTT TCT ATT TKD 337
 Lys Pro Leu Leu Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa

| | | | | |
|---|-----|-----|-----|-----|
| | -20 | -15 | -10 | |
| ACT CTK CTT TGG GGC TTG AAC TGT AAG AGG TCC TGG AAC ATA AAT TTG | | | | 385 |
| Thr Leu Leu Trp Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu | | | | |
| | -5 | 1 | 5 | |
| AGA ATT GTT GSA TCA TAC AGT ACT GGT TAC | | | | 415 |
| Arg Ile Val Xaa Ser Tyr Ser Ser Gly Tyr | | | | |
| | 10 | 15 | | |

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..133
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq RLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

| | |
|---|-----|
| AGAGGCAACC ATG GCG GGA GGA ATG AAA GTG GCG GTC TCG CCG GCA GTT | 49 |
| Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val | |
| -40 -35 -30 | |
| GGT CCC GGG CCC TGG GGC TCG GGA GTC GGG GGC GGT GGG ACA GTG CGG | 97 |
| Gly Pro Gly Pro Trp Gly Ser Gly Val Gly Gly Gly Thr Val Arg | |
| -25 -20 -15 | |
| CTA CTC TTG ATC CTC TCC GGC TGC TTG GTC TAC GGC ACA GCT GAA ACT | 145 |
| Leu Leu Leu Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr | |
| -10 -5 1 | |
| GAT GTA AAT GTG GTC ATG CTT CAG GAA TCC CAA GTT TGT GAA AAG CGT | 193 |
| Asp Val Asn Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg | |
| 5 10 15 20 | |
| GCC AGC CTC GCG | 205 |
| Ala Ser Leu Gly | |

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 58..153
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ACTTCCACGG GACCCACCAG CTAAATGCC GGCAGCCCTG GGAATTCTGG CCTCACA      57
ATG GTT GAG ATG ACT GGG GTG TGG CAG TGC CAA GCC GAG GCT GTG AAA      105
Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys
      -30                      -25                      -20

GGC CTT CCA CCT TTA CTC TCG TGC TCG TGC CCT CCC CCA TTG TTA GGA      153
Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly
      -15                      -10                      -5

GAA GGG CAT GCT CAG GCC AGC CCA TTA GCC CAG GAG GAG GAC AAG AAA      201
Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys
      1                      5                      10                      15

CAC ACG GAG CAG ACA CAA GCC ACC TCA CCA ACC CAG CCT      240
His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 59..121
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq AGLLP LLLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

AATTTGCTCA CACCCAGCAG GCAGAGAAGG CAGCAGCAGG CAGGACCGCC ACCCTCCC      58
ATG CAA ATC ACC CCC GGG AGT GCA GCT GGG CTC CTC CCG CTC CTC CTA      106
Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu
  -20                      -15                      -10
GGC AAT GCT CCT GGG GAG TCT GTT GGG GGA AGA TGC SAT CCA GGG TGC      154
Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys
  -5                      1                      5                      10
TGG
Trp

```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 152..202
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq TWLLLT LQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

AGAATTTTGC TGGGAATTAA TATTAAATAC TCACTGGAAT TTATCTTTAC CAACTTTAGT      60
GGAATTCAGC CTATCTACAG CTCTCCTTTC CACTTTGTTT CTCAGAAATT CTCAGCAATG      120
GTTTCATGAA CCACTGGGAG GTCATTGCCC T ATG ATT TTG TCC ACC TGG CTC      172
Met Ile Leu Ser Thr Trp Leu
                      -15
TTA CTT ACC CTT CAA AAC TCA GTA TTT ACA TCT TTC AGG ATA TCT CCC      220
Leu Leu Thr Leu Gln Asn Ser Val Phe Thr Ser Phe Arg Ile Ser Pro
-10                      -5                      1                      5
AAC AGA ATA CAA AGT ATG CTA CCT CCC ATG
Asn Arg Ile Gln Ser Met Leu Pro Pro Met
  10                      15

```

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..128
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VCIVLALCHTSRP/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

AAATCTCTTC TAATCCTCCT TAATGCATTT TG ATG GCT TTT CAT AGC TAT TGG      53
                               Met Ala Phe His Ser Tyr Trp
                               -30

GGA AAA AGT TTA CAA TCC TTT AAG ACG TTC ATG AGA GTC TGC ATT GTC      101
Gly Lys Ser Leu Gln Ser Phe Lys Thr Phe Met Arg Val Cys Ile Val
-25                -20                -15                -10

TTG GCC CTT TGC CAC ACA TCC AGA CCC ATG TCT TAC CAT GTT CCC CTG      149
Leu Ala Leu Cys His Thr Ser Arg Pro Met Ser Tyr His Val Pro Leu
                -5                1                5

GCT GCT GGC TCC CCA CTC ATG CAC TGG TCT CCT TGT AGT CCT GTG CCC      197
Ala Ala Gly Ser Pro Leu Met His Trp Ser Pro Cys Ser Pro Val Pro
                10                15                20

TTC ATT GGG
Phe Ile Gly
                25

```

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 113..160
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq RFTLLPLVLHSQS/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

ATTCTCGTA AATGATGAGA TGGGGTTAAA TGTTTTGCA GAAATATGTG AGAGGTAATG   60
TGAAATAAGT TACTTTAAGA AGGCCTGGCC CTGGTAATGT CATTACCAGC TG ATG AAG   118
                                         Met Lys
                                         -15

TTG CGG TTT ACC TTG CTG CCC CTG GTG CTA CAT TCA CAA AGC AGC TGT   166
Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser Ser Cys
          -10                      -5                      1

GTC TTT TGG AAA GCC GGG                                           184
Val Phe Trp Lys Ala Gly
          5

```

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 4..93
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FIPFLVIY3FVLS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

ACC ATG ATG ATC ATT CTG GGG TTT GCT TTT TGC CCT GGT CAC TTT AGG   48
Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg
-30                      -25                      -20

TTT AAT TTT ATT CCA TTC CTG GTC ATT TAC AGT TTT GTT CTG TCA TCT   96
Phe Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser
-15                      -10                      -5                      1

CCC CAT ACC CAT CGA GAA CCC TAT TCT CCT GTG GCA GAC TTT AAT GAA   144
Pro His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu
          5                      10                      15

```

(B) LOCATION: 396..405
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name CREL_01
 score 0.962
 sequence TGGGAATTCC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: 423..436
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name GATA1_02
 score 0.956
 sequence TCAGTGATATGGCA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: complement(478..489)
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name SRY_02
 score 0.951
 sequence TAAAACAAAACA

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: 486..493
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name E2F_02
 score 0.957
 sequence TTTAGCGC

(ix) FEATURE:

(A) NAME/KEY: TF binding-site
 (B) LOCATION: complement(514..521)
 (C) IDENTIFICATION METHOD: matinspector prediction
 (D) OTHER INFORMATION: name MZF1_01
 score 0.975
 sequence TGAGGGGA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

TGAGTGCAGT GTTACATGTC AGTTGGGTTA AGTTTGTTAA TGTCATTCAA ATCTTCTATG   60
TCTTGATTTG CCTGCTAATT CTATTATTTT TGGAACTAAA TTAGTTTGAT GGTTCTATTA  120
GTTATTGACT GAGGTGTGCT AATCTCCCAT TATGTGGATT TATCTATTTT TTCAGTTGTA  180
GATAGGACAT TGATAGATAC ATAAGTACCA GGACAAAAGC AAGAGATCT TTTTCCAAA  240
ATCAGGAGAA AAAAATGACA TCTGGAAAAC CTATAGGGAA AGGCATAACA GATGGTAAGG  300
ATACTTTATC TTGAGTAGGA GAGCCTTCCT GTGGCAACGT GGAGAAGGGA AGAGGTCGTA  360
GAATTGAGGA GTCAGCTCAG TTAGAAGCAG GGAGTTGGGA ATTCCGTTCA TGTGATTTAG  420
CATCASTGAT ATGGCAAATG TGGGACTAAG GGTAGTGATC AGAGGGTTAA AATTGTGTGT  480
TTTGTTTTAG CGCTGCTGGG GCATCGCCTT GGGTCCCCTC AAACAGATTC CCATGAATCT  540
CTTCAT                                     546

```


TGT AAC CGC AGT
Cys Asn Arg Ser
20

156

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 198..278
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```

AACTTTGCCT GGGTGTCTTG CGTTCTGCAC ATTCCGGAGG ACCAGCTTCC CCATCAGAAG   60
TCTGACTCCA TGGAAACCAG ATGGGGCAAC GGGGTGGTTC TACTGCAGAC TGTAGCTGCA   120
GCTCCTCTCC ACCTCTAGCC TGCTCATTTT CAGCTCAGAA ATTCTACTAA TGGCGTTTTT   180
TCTTCTTGAA AAAGGAA ATG AAC AGG GTC CCT GCT GAT TCT CCA AAT ATG   230
      Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met
      -25                      -20

TGT CTA ATC TGT TTA CTG AGT TAC ATA GCA CTT GGA GCC ATC CAT GCA   278
Cys Leu Ile Cys Leu Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala
      -15                      -10                      -5

AAA ATC TGT AGA AGA GCA TTC CAG GAA GAG GGA AGA GCA RRT GCA AAG   326
Lys Ile Cys Arg Arg Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys
      1              5              10              15

ACG GGC GTG   335
Thr Gly Val

```

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 195..239
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

AATATGTAAA TGTACTATAC AGAATTATAC ATAAAAGAGA AACTTTTCAT GTATGTAAGT   60
TAAAAAATGA AGTAAATGGG GGTTCCAAAT AACATTARAA TEGGTTATGA GTTTTGTAAA  120
AGGAAATCAT ACTTGGCATT CTAAACTTAA TATTCTTTTG CAATGTTTAG GTATATGTGG  180
ATATTCCTGG AGCT ATG GAT TTA TTT CTT AAT TTG CCA CTT GTC ATC GGT   230
      Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly
      -15                -10                -5

ACC ATT CCT CTA CAT CCA TTT GGT AGC AGA ACC TCA AGT GTA AGC AGT   278
Thr Ile Pro Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser
      1                5                10

CAG TGT AGC ATG AAT ATG AAC TGG CTC AGT TTA TCA CTT CCT GAA   323
Gln Cys Ser Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu
      15                20                25

```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..229
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

| | |
|---|-----|
| AAAAATATTAA ATG GMA AAA AAT CAC AGA AAT AAA AAA TCC ATA CAT TTT | 49 |
| Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe | |
| -70 -65 | |
| CCA CTG TGC ACC ATT CCA AGT AGM ATG MTG AAA TCT TGT ACT CTC CCA | 97 |
| Pro Leu Cys Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro | |
| -60 -55 -50 -45 | |
| CTT CAG CGC ACC TGG GAC ATS MAT CCT TCC TTT GTC CAT TGG AWC CAA | 145 |
| Leu Gln Arg Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln | |
| -40 -35 -30 | |
| GCC CGY CTA CAA TCC CCA CCG YCT AGT CAC TTA GTA SCC CTC TCG GTG | 193 |
| Ala Arg Leu Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val | |
| -25 -20 -15 | |
| ATC AGA TCG ACT CTC GTG CTA TCC CAG TGC TTG TGT TCA AGG MAC CCT | 241 |
| Ile Arg Ser Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro | |
| -10 -5 1 | |
| TAT TTT AGT GCA ATG ATG ACC CCA AAG TGC AAG AGT ATT GMT GCT GGC | 289 |
| Tyr Phe Ser Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly | |
| 5 10 15 20 | |
| AAT TCA GGT ATG CCA AAG AGA AAC TGT AAA GTG CTT CCT TCA AGT GAA | 337 |
| Asn Ser Gly Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu | |
| 25 30 35 | |
| AAG ATG MAA GTT CAC | 352 |
| Lys Met Xaa Val His | |
| 40 | |

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 317..358
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SFIALVYSSLSEQ/KV

SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

AGAGCAAAGC AGACAGAAAT TCCTCTGGTT CTGTAGAGCT GACAATTCAT TAATGTGAGG   60
TAGTCAATAA CAAATATATT TTATGTCAAG TGGTGRATGG DTYCDATTGA AGAAAAATGA   120
CTCAATAAGA GGAGAGAAAA TGATGGTATG TGTATGGTGG GTAGGTGTGC GTGATGCTGT   180
TTTGGATAGC GAGGCCTCCG ATTAGATGCT ACGTGAGCAG GGACCCAAAA GAGCCATGTG   240
TTTCATCTAC CTGGGGGAGA AGCCTGCTGG CAGATCCTGT TGAACACTCG TTACCTAAAT   300
CTCTTGCATT GGCTCC ATG TCA TTT ATT GCT CTA GTG TAT TCT TCA CTA TCT   352
          Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser
                    -10                                -5

TTT CAG AAA GTG CCA GGG
Phe Gln Lys Val Pro Gly
          1

```

370

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 93..158
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

ATAATATAGA TCITTAATTT CTCTCAGCAA TGATTATAGT TCACAATGTG GAGGATTTAC   60
ATGTCCTTCA TTAAATTTAT CCAAAGTACT TT ATG GTT TTT GAT ACT TTA AAA   113
          Met Val Phe Asp Thr Leu Lys
                    -20

AGT ACA ATT GTT CTT TTT TTA AAT TCG RWT TTC CCA ATC ATT TGC AGC   161
Ser Arg Ile Val Leu Phe Leu Asn Ser Xaa Phe Pro Ile Ile Cys Ser
-15          -10          -5          1

CGG
Arg

```

164

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 68..244
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq IFLFSILLMSLRT/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

AAAGCACAGA TGGCACTCCA TTCATTGAAG ATGGTTTTTT TCAAGGTGAG TGTGGTCTT   60
TTGCACA ATG CTT GAG ATG GAA ATG ACT TGG CTG AGA CTA TGT GAT GAG   109
      Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu
                        -55                      -50

TGC TCC AGA TGG GGC ATG GCA TCG GCA TGG GGT AGG GGT GGA AAG CTT   157
Cys Ser Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu
-45                      -40                      -35                      -30

CTT GGA GCT CAA GTA GCC CTT CAT CCT AGA AAC TGC AGC AAA GCT AAG   205
Leu Gly Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys
      -25                      -20                      -15

ATC TTC CTG TTC AGT ATT TTA TTA ATG TCT TTA AGA ACT TTT CAC TGT   253
Ile Phe Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys
      -10                      -5                      1

AAT TAT TTC AGA GGC AAT GGG   274
Asn Tyr Phe Arg Gly Asn Gly
      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 104..154
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq MLFFLGALCRESG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

AACAAAGGAG GGAAGGGTTA GAGTGAGGTA CTCACCCAGA GAAGAGCTGT CCCGGCCTGG      60
GGGTCCCATC CGTCCCTTCT CTTTCTTGCC AAAGAGACGG CCT ATG GAT GAC TTG      115
                               Met Asp Asp Leu
                               -15
ATG CTC TTC TTC TTG GGG GCT TTG TGC AGA GAA TCT GGG GTG CCC TCA      163
Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser Gly Val Pro Ser
      -10                -5                1
CTG GGA AAG CAG GAG AGA ATG AGA GCA TAT GCT GCT GAG ATG CCC CCT      211
Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala Glu Met Pro Pro
      5                10                15
CTC CTC CCA AGT CCT TGT CCA CCC CCT TCT CAT CTT CCC AAG CCA GCT      259
Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu Pro Lys Pro Ala
      20                25                30                35
TCT CCC TGT CCC TAT CCC TTG NNC CTG CTG ACC TTC CCC GTG GGG GTC      307
Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe Pro Val Gly Val
      40                45                50
CCC CAT CTT CCA GGG ACC CGC CTG CAG TGC CAA GTC CTG GGT CAT TCT      355
Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly Leu Gly His Ser
      55                60                65
CTC ARA CGG GCA GAG CGG GGA GTG GGT GGT GGG GTG TCT CCT GGG      400
Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val Ser Pro Gly
      70                75                80

```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 13..87
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq LPTLLLLPVGAPG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

ATCGAATGCA GA ATG GTT TTG GGA GCC CTG AAC CTT CCC TCC CAG GAA CTC   51
      Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu
      -25                      -20                      -15

CCC ACT CTC CTG CTC CTC CCA GTG GGG GCA CCT GGR AAG AAA AAA GGC   99
Pro Thr Leu Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly
      -10                      -5                      1

ATG GAA GGC AAA ACT CCC TTG GAC CTG TTT GCT CAT TTT GGC CCT GAG   147
Met Glu Gly Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu
      5                      10                      15                      20

CCA GGG GAC CAC TCA GAT CCG CTG CCT CCC TCT GCA CCC TCT CCC ACT   195
Pro Gly Asp His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr
      25                      30                      35

CGG GAG GGG GCT CTG ACC CCG CCC CCA GGG   225
Arg Glu Gly Ala Leu Thr Pro Pro Pro Gly
      40                      45
  
```

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 207..263
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq QTFVSFSLIPVLG/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

ATACAGCTCC ATTTTAAATG TGCTGCAATA TGAATGAAGT GACCTGTGTT TCATCACTTG   60
TTCAATGAT TCTTATCCAT GTTTTGTAC TTAGTAAGGG CCATACGTAG TGGGATTAAA   120
TATTGTGCC CTTGCTTTGA AAACAAAAC TAAAGTGAAT GACACATAAG GGCAGGGATT   180
  
```

TCAGAACAGA TTTTCTTGA ATAAAA ATG CTT GTG TCA AAA ATT CAA ACA TTT 233
 Met Leu Val Ser Lys Ile Gln Thr Phe
 -15

GTC TCT TTC CTT TCC ATT CCA GTT CTA GGT CTC GTT CCA GAT CAT ATT 281
 Val Ser Phe Leu Ser Ile Pro Val Leu Gly Leu Val Pro Asp His Ile
 -10 -5 1 5

CTC CAG CTC ATA ACA GAG AAA GAA ACC 308
 Leu Gln Leu Ile Thr Glu Lys Glu Thr
 10 15

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 188..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
 seq LLSTGLNILGTQA/FR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATCATAGTCA CTTTCCAAGT TTATGACCCA GAGCAATCTG ACCTTGGTAG CTTGTCTCCC 60

TCATTAAATT CTCTGACTTC ATAATCAGCT CACATTCCTT TCCTCTCTTT CCCTCTCTTT 120

TTAAATATCT GTAAACATT CAAATTGATC CACGTAGATT TATCTTGCTT TTAGGCCACA 180

CTCTGAG ATG TGT AAT CCG GTT GCT CAC ACA TTT AGA GGA GTC CAT GAG 229
 Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu
 -30 -25 -20

CAT CAC GCC ATG CTA CTC TCC ACT GGT TTG AAC ATC TTA GGC ACT CAG 277
 His His Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln
 -15 -10 -5

GCA TPC CGT TAC GAA GAT GGG CAG CTG 304
 Ala Phe Arg Tyr Glu Asp Gly Gln Leu
 1 5

(1) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 126..176
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq ILLWEACTGRCQA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

TATTCAGTTG GGGGCAAGCC AGCCATGATG TGGACCTTTC ATTGGGTAGG GCAAGTCCCC   60
AAAGTTGGAA AAATGGAAAG TGGGAGCTGT GAGGCACGTG TTACACCCAC ACTTTCCTCC   120
TACAG ATG CAG TGT TGG ATT TTG TTG TGG GAG GCA TGC ACA GGT AGG TGC   170
    Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Lys Thr Gly Arg Cys
        -15                -10                -5

CAG GCC TCC CTA CTC TCT CCC TGG CCC AGA GGT GGC AGG GGC AAG TTA   218
Gln Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu
        1                5                10

GTG GCA GTG GTG GCT GCA AAA TGG TTG GCA GCA ATC TGT GGG ATT TGG   266
Val Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp
    15                20                25                30

GCT ATC AAA GAA ATG CCA AGC CAT GGC CAC AGT CTT CAA GCA GGG GCA   314
Ala Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala
        35                40                45

GGG GAA GGT GCA CTG GTG ACC TGG AGC CTG CAA ACC TCA TTT GGT GTG   362
Gly Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val
        50                55                60

AAG CAG TAT AAG TGG GGA GTT GTG TGG CAT GAA GCA AAC CTG TTG CTT   410
Lys Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
        65                70                75

```

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 149..223
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

ATTTTAGAAA GTAAGGAAAT AAAACTTTAA TTGAAGTTGG AATAAACTCA GTTCTGAGCA    60
TTCCATTCTA CTCTGCAGTT GTCATTATA GACAGCTGTG GATCATAATA CCTATAGACT    120
AGATATCGTT ATCTACTTAT TTATATTA ATG ACA GGA TAT CCC TGG GCA AAC    172
                        Met Thr Gly Tyr Pro Trp Ala Asn
                        -25                      -20

AGC ATC ACC ACT GTA CTG TGT ATT CTT GGT TGT CAT GGG AAC CTT TGC    220
Ser Ile Thr Thr Val Leu Cys Ile Leu Gly Cys His Gly Asn Leu Cys
      -15                      -10                      -5

TGT GAA CCA GCA GTG AGA GCA CTC GGG                                247
Cys Glu Pro Ala Val Arg Ala Leu Gly
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 561 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 475..546
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IFTALFLXLHSA/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

AAATTATGGA TGCCTACCAT CTACCAGGTA CTGTTCTAGC TACAGGAAT AACTAAAAAT    60

```

AGGTAAACAA AACAGATGAA AAACCTAGAA ATTTATACTG ATGTTATCAG AGTAATGTTT 120
 AATTTTTCAG ATAATTGTTA TGTCTAAATT AGCATTGAT TTTTCAATTA AGAATTTTTA 180
 AATTATCCAA TATTGCAAGC ATATATAGAA ACATGGAAAA CAACAAAATT CTCATGCATA 240
 TACTTCAAAC ACAGAGCTAA CAGATGTTAT TATTTTTTAT TTCTTTCACA ACCCAACTTT 300
 CGGGAAACAA AATAGGCACA GCAAACTGG GATCTCCTCA TCCCCTTCTC CTTTCTTATA 360
 TAAAAGTAAT CCGTCTCTTG GTACAGCTAT GTATCATACT CATCCAGGTT TTAATTTTTC 420
 TTATATAACG GAACATATAT GGTGTTATTT TACGGATTTT AAAGCTTTAC ATAA ATG 477
 Met
 GTG TCA TGT GAT GTW CVN TCT TAT GTG ATC ATT TTT ACT GCA CTC TTT 525
 Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu Phe
 -20 -15 -10
 TTA WTG CTG CAT AGT GTG GCA ATA AAT GAA GAG TTT 561
 Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..139
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ATGATAAGGG CTTATTCACA TTATTCATTC TTGAATGAAT TTGATAGTG TCTGTCTTTC 60
 AGGAACTTTG TCCTAAGTA ATG AAA TCC TTT GAT AAA AAG TTG TTT GCA ATA 112
 Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile
 -20 -15 -10
 TTT CTT ATG TGT TTA AAG TCT ATA GGT TCT GTG GTG ATG CCC CAG CCG 160
 Phe Leu Met Cys Leu Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 36..134
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

ATTTCCTCC CCGCAACCTG GTGAAAGCCA AYKCA ATG TTC GGT GCG GGG GAC      53
                               Met Phe Gly Ala Gly Asp
                               -30

GAG GAC GAC ACC GAT TTC CTC TCG CCG AGC GGC GGT GCC AGA TTG GCC      101
Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser Gly Gly Ala Arg Leu Ala
-25                               -20                               -15

TCA CTT TTT GGA CTG GAT CAG GYA GCY SST GGC CAT GGA AAT GAA TTT      149
Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa Gly His Gly Asn Glu Phe
-10                               -5                               1                               5

TTC CAG TAC ACA GCC CCA AAA CAG CCT AAG AAA GGC CAG GGA ACG GCA      197
Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys Lys Gly Gln Gly Thr Ala
10                               15                               20

GCA ACA GGA AAT CAG GCA RCA CCA AAA ACA GCA CCA GCC RSC ATG AGC      245
Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr Ala Pro Ala Xaa Met Ser
25                               30                               35

ACT CCC ACA ATA CTG GTC GCA ACA GCA GTC CAT GCA TAT CGA TAC ACA      293
Thr Pro Thr Ile Leu Val Ala Thr Ala Val His Ala Tyr Arg Tyr Thr
40                               45                               50

RAT GGT CRA TAT GTA AAG CAG GSR AAT TTG GTG CTG CAG TTC TGG      338
Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu Val Leu Gln Phe Trp
55                               60                               65

```

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 107..190
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RFLSLSAADGXDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

AAAGTCAGCG CTGGAGTCGG CTAGGCGGCT GGAAACGGCG GCTGCCGCCG GTGACTCAGG 60
GAGGCGGGAG GCGMSGGMG GAGCTCTTCC TGCAGSCGTG GARACC ATG GTG CTC 115
                               Met Val Leu
ACG CTC GGA GAA AGT TGG CCG GTA TTG GTG GGG AGG AGG TTT CTC AGT 163
Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser
-25                -20                -15                -10
CTG TCC GCA GCC GAC GGC ASC GAT GSC AGC CAM GAC AGC TGG GAC GTG 211
Leu Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser Trp Asp Val
                -5                1                5
GAG CGC GTC GCC GAG TGG CCC TGG CTC TCC GGG ACC ATT CGA GCT GTT 259
Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val
                10                15                20
TCC CAC ACC GAC GTT ACC AAG AAG GAT CTG AAG 292
Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys
                25                30

```

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 361..411

- (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

ATGAAAACAG TTTTCTTTGT GATTGTGCAA TTGATGTTTA AACAGTGTTT ATCCTTCCAG   60
GTAGTATGAT GATGTATTTG TTGGAGACAA ARTATTTGCC CTAGCCTTTT TACTAATATT  120
TCAGATGAGA TTCTGTGGAG GAGAAGCATC TCCCCAAATG TCCTTGTTTT ATAGTAAATA  180
ATTCTACCAC GAGGATCCTT ATCCATAAAT CTATATTCAT GTTATTTTGG TGCTAGATAC  240
AGATCTTGCA ATATTCATGA AGCTTTAAGA AGAGCACTTT GAATCTTAAA AGAGATTCTC  300
TGAGCAGGGG TTGGCAGTGG TGAGGTCCAG GTAGTTATAA TAGCCATAAG AGCAGGGATT  360
ATG GTT ATT GAG CTC ACC AGT GTG TTT CAA GCC ATG ATC TGG AGT CAA   408
Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln
      -15                      -10                      -5

GGT GTT AGT GAT TCC TCT AAG
Gly Val Ser Asp Ser Ser Lys   429
      1                      5
  
```

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 47..196
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

ATDCCGCCCT GGAGCAAGCC GGGGCCTGGT CGGCARCTGG GCGGCC ATG GAG TCC   55
                                     Met Glu Ser
                                     -50

ACG CTG GGC GCG GGC ATC GTG ATA GCC GAG GCG CTA CAG AAC CAG CTA   103
Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln Asn Gln Leu
      -45                      -40                      -35
  
```

GCC TGG CTG GAG AAC GTG TGG CTC TGG RRT SAC CTT TKC TNG SCG ATC 151
 Ala Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa Xaa Xaa Ile
 -30 -25 -20

CCA AGK ATC CTC TTT CTG TTC TAC TTC CCC GCG GCN TAC TAC GCC TCC 199
 Pro Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr Tyr Ala Ser
 -15 -10 -5 1

CGC CGT GTR GGC ATC GCG GTG CTC TGG ATC AGC CTS ATC ACC GAG TGG 247
 Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile Thr Glu Trp
 5 10 15

CTC 250
 Leu

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 196..270
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
 seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATNCTGTGTT ACTCATTTCC TGTCTCAGAT ACTTTGGATC CTTGGTTCT GATCTTTCAG 60

GGGGAGAGGG CATGTTAAGA GGAGTAAGTA GATGGATGAT CTTACACAAT TGAACCTTTC 120

TTACCTCTGG CTTGTATGC TCTTACATAG GCTGTCCCCT CTCTACATTT TCTTATTTAA 180

GGAAAAACAC AGAAC ATG ATT ATT GTC TCA GAA TTA GSA ACC CCT ACT GGT 231
 Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly
 -25 -20 -15

GTG CTC GTA GGT GTC TTT TTG TCT ACT TTT CTC TAT TGT GAA TGT GTA 279
 Val Leu Val Gly Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val
 -10 -5 1

AAG GGG CCG 288
 Lys Gly Pro
 5

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..145
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq GFLLCPLVCGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

AGCGTTTATG GCCGCGTTAA GTCTGAGTGC CGCTTTGAGT TGTGGAATGA AGTGAAC TTC      60
ATTGTGTCAGC GTTCGGTTC ATG AAC TGG AAT GTA AGA TGC ACC AGA GGA TTC      112
               Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe
               -20                               -15

CTG CTC TGT CCC CTG GTT TGC GGC TTG CGA CGT TGG ACA TCC CCG GAT      160
Leu Leu Cys Pro Leu Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp
-10              -5              1              5

TGT TGT TTA ATA GAG AAA ACT CAC CGC GGG                                190
Cys Cys Leu Ile Glu Lys Thr His Arg Gly
              10              15

```

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 49..105
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq RGLLLGLAVAAAA/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

AAGATAGAGG CGGCAACCTC GGAAGTGCGG ACGGGTGGGC CTATATAG ATG TTG AGG      57
                                         Met Leu Arg
TGC GGA GGC CGT GGG CTT TTG TTG GGC CTG GCT GTA GCC GCA GCA GCG      105
Cys Gly Gly Arg Gly Leu Leu Leu Gly Leu Ala Val Ala Ala Ala Ala
  -15                               -10                               -5
GTA AGG
Val Arg
1

```

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 95..136
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq ILLMIVFSIFLLL/CN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

ACCCAGAGGC AGAAAGTAAT ATTGCTTACT ATGAGTCTAT ATATCCTGGG GAATTGAAGA      60
TGCCAAAGCA GCTCATTAC ATACAGCGTA AGTA ATG ATT CTC TTA ATG ATT GTA      115
                                         Met Ile Leu Leu Met Ile Val
                                         -10
TTT TCT ATA TTT CTC TTA TTA TGT AAC TTG ACA GAT TTT TAT CTC TTC      163
Phe Ser Ile Phe Leu Leu Leu Cys Asn Leu Thr Asp Phe Tyr Leu Phe
  -5                               1                               5
AGG AGC GAT GGG
Arg Ser Asp Gly
10

```

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 149..190
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq SLLFIFRSILISC/FS
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
ACAATTTGTT TTATAAGCCT ATATTAATTG GGTTTTGACT GAATTAATTA TATAACCATT    60
TATCTCAAAA TGAAATGTTT CATAAAATTT ATTTAAWAGT ATATACTGYA TAAGTGTTAA    120
ATTATGAAAT TTAGTGGTCT TATAGAGA ATG TCT TTA TTG TTT ATT TTT AGG      172
                               Met Ser Leu Leu Phe Ile Phe Arg
                               -10

TCA ATT TTG ATC TCC TGC TTT TCA GGA GAC TTT TTT TTT TTT              214
Ser Ile Leu Ile Ser Cys Phe Ser Gly Asp Phe Phe Phe Phe
-5                               1                               5
```

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 27..77
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq SKVLIQLSQAFWA/SP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

ACCTGGTATG AATTACAAAA CTGTAA ATG CCT TTG ATT AGT AAA GTT TTG ATA 53
 Met Pro Leu Ile Ser Lys Val Leu Ile
 -15 -10

CAG CTA AGC CAA GCA TTT TGG GCC TCA CCT GAG GGT AGG AAC AGT TCT 101
 Gln Leu Ser Gln Ala Phe Trp Ala Ser Pro Glu Gly Arg Asn Ser Ser
 -5 1 5

GGG AGT AAG AGG AAG CAG TTG GTA GCT GCA GTG GAG ATG CGA TAC TGT 149
 Gly Ser Lys Arg Lys Gln Leu Val Ala Ala Val Glu Met Arg Tyr Cys
 10 15 20

AAA AGG CAG CAG GGG 164
 Lys Arg Gln Gln Gly
 25

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 142..228
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
 seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AAGTTGTAAT CCCACTAAGA ACCGCCAGGG CGAGACGAAA GCGACATCGC TTCCATCTTT 60

ACGACCAAGA ATCGCCTTCA GCCCTGTCTG GTGCATCCTT GACAGAAAGT GAGGAGGAA 120

ACACCCCCAT TGTTCTTTGG C ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA 171
 Met Asp Thr Ser Ser Val Gly Gly Leu Glu
 -25 -20

TTG ACT GAT CAG ACT CCT GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT 219
 Leu Thr Asp Gln Thr Pro Val Leu Leu Gly Ser Thr Ala Met Ala Thr
 -15 -10 -5

AGT CTC ACG AAT GTA GGA AAC TCA TTT ACT GGT CCA GCT AAT CCT TTA 267
 Ser Leu Thr Asn Val Gly Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu
 1 5 10

GTG TCT AGA TCT AAT AAG TTT CAG AAC TCG TCA GTG GAA GAT GAT GAT 315

Val Ser Arg Ser Asn Lys Phe Gln Asn Ser Ser Val Glu Asp Asp Asp
 15 20 25
 GAT GTT GTT TTT ATC GAA CCT GTA CAA CCT CCC CCA CCT TCT GTA CCA 363
 Asp Val Val Phe Ile Glu Pro Val Gln Pro Pro Pro Pro Ser Val Pro
 30 35 40 45
 GTG GTA GCT GAT CAA AGA ACC ATA ACA TTT ACA TCA TCA AAA AAT GRA 411
 Val Val Ala Asp Gln Arg Thr Ile Thr Phe Thr Ser Ser Lys Asn Xaa
 50 55 60
 GAA CTA CAA GGA AAT GAT TCC AAA ATT ACT CCT TCC TCA AAA GAG TTG 459
 Glu Leu Gln Gly Asn Asp Ser Lys Ile Thr Pro Ser Ser Lys Glu Leu
 65 70 75
 GCA TCT
 Ala Ser 465

(2) INFORMATION FOR SEQ ID NO: 158:

--(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..184
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq ILLLTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

ACACACGTCC CGCMGTGGAT ACTGGAGAAT CCTGCCACA CACGTCCTGC CGTGGACACT 60
 GGAGAATCCT TCTCGCCACA CACTTCCCAC C ATG GAC ACT GGA GAA TCC TTC 112
 Met Asp Thr Gly Glu Ser Phe
 -30 -25
 TCG CCA CAC ACG TCC TGC CGT GGA CAC TGG AGA ATC CTT CTA CTC ACA 160
 Ser Pro His Thr Ser Cys Arg Gly His Trp Arg Ile Leu Leu Leu Thr
 -20 -15 -10
 CAC GTC CCA CCG TGG ATA CTG GAG AAT CCT TCT TGC CAC ACA CGT CCC 208
 His Val Pro Pro Trp Ile Leu Glu Asn Pro Ser Cys His Thr Arg Pro
 -5 1 5
 GCC GTG GAC ACT GGA GAA TCC TTC TCG CCA CAA CCG 244
 Ala Val Asp Thr Gly Glu Ser Phe Ser Pro Gln Asn
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 154..246
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

```

ATAGGACTGC TACAAAAACC CCATGTTTAC GAATTGCCA GTGATATTGC CCCCTTCCTG   60
TGTCATCCCA ATTTATGGAT ACGTTATGGT GCCGTGGGAT TTATCACAGT GGTAGCTCGT  120
CAAATAAGTA CAGCTGATGT CTACTGTAAA CTG ATG CCT TAT CTT GAC CCA TAT   174
                               Met Pro Tyr Leu Asp Pro Tyr
                               -30      -25
ATT ACC CAA CCA ATA ATA CAG ATT GAA AGA AAA CTT GTT CTG CTC AGT   222
Ile Thr Gln Pro Ile Ile Gln Ile Glu Arg Lys Leu Val Leu Leu Ser
                               -20      -15      -10
GTT TTA AAG GAA CCA GTA AGT CGT TCT ATA TTT GAT TAT GCT TTG AGG   270
Val Leu Lys Glu Pro Val Ser Arg Ser Ile Phe Asp Tyr Ala Leu Arg
                               -5              1              5
TCT AAA GAT ATT ACT AGC TTG TTC AGA CAT CTT CAC ATG CGT CAG AAG   318
Ser Lys Asp Ile Thr Ser Leu Phe Arg His Leu His Met Arg Gln Lys
                               10              15              20
AAA CGA AAT GGT TCT CTT CCC GAC TGC CCT CCG CCA GAG GAT CCT GCC   366
Lys Arg Asn Gly Ser Leu Pro Asp Cys Pro Pro Pro Glu Asp Pro Ala
                               25              30              35              40
ATA GCA CAG CTT CTG AAG AAG TTG CTC TCA CAG GGA ATG ACA GAG GAA   414
Ile Ala Gln Leu Leu Lys Lys Leu Leu Ser Gln Gly Met Thr Glu Glu
                               45              50              55
GAG GAA GAC AAA CTT CTG GCA CTG AAA GAC TTC ATG ATG               453
Glu Glu Asp Lys Leu Leu Ala Leu Lys Asp Phe Met Met
                               60              65

```

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 181..267
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```

ARRAAAGCCG GGACTGGACC GAGCGGAGTK KTGCGTGTCG CCGAAGGGGG GTKGCCCGGG   60
GGAGGKGAGG TTCGTTCCGC GGA KCCGCAG YCAGAASCGK GRACCAAGAA TCGCCTTCAG   120
CCCTGTCTKG TGCATCCTTG GCAGAAAGTG RKGAKGAAAA CACCCCCATT GTTCTTTGGC   180
ATG GAC ACA AGT TCA GTG GGA GGA TTA GAA TTG ACT GAT CAG ACT CCT   228
Met Asp Thr Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
      -25                      -20                      -15

GTT TTA TTA GGG AGT ACG GCC ATG GCA ACT AGT CTC ACG AAT GTA GGA   276
Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
      -10                      -5                      1

AAC TCA TTT AGT GGT CCA GCT AAT CCT TTA GTG TCT   312
Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser
      5                      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 33..116
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq FGLLDFVQCCDS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```

ATTTTTATG ACATCTAWTT ATATTGAGTT GC ATG CAT GTT TTG TTC AAC ATA      53
                               Met His Val Leu Phe Asn Ile
                               -25

GTC ACA ACA AAT WRR RAT AAC CAT TTT GGG TTG TTA CAT TTT GTT GTG      101
Val Thr Thr Asn Xaa Xaa Asn His Phe Gly Leu Leu Asp Phe Val Val
-20                               -15                               -10

CAG TGT TGT GAT TCA TTA AGA AAC CAT ARG WGG TCA TTT CAG TCA TCT      149
Gln Cys Cys Asp Ser Leu Arg Asn His Xaa Xaa Ser Phe Gln Ser Ser
-5                               1                               5                               10

TAC TTG AGG CTA AAT CAT TCA TGR CAT ACA TGT                          182
Tyr Leu Arg Leu Asn His Ser Xaa His Thr Cys
15                               20

```

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 150..215
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq TAYWLSFMSWAQS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

```

ATGTATACTG AGGTTTCAGGA ACTGCTGGAG AGATGACTGG GCACCAAGAG GATGACAGTG      60

ACTCAGCTGG CATCCCTTAG CTGGTTCATG GCAGAGCTGA GTGGCCACTC CTGTCTCTGA      120

CCCCAGCTTC AGTGCTCTTT ATCTCCTCC ATG CCT CCT CAG TCG TGC TGC TCT      173
Met Pro Pro Gln Ser Cys Cys Ser
-20                               -15

```

```

AAG ACT GCT TAC TGG CTT TCC TTC ATG TCC TGG GCA CAG AGC AGT TCT      221
Lys Thr Ala Tyr Trp Leu Ser Phe Met Ser Trp Ala Gln Ser Ser Ser
          -10                      -5                      1

TTT GGT AGC AGA HTT GAG TCC ACT TCC CCC TGC ACA GAT CAC TGC TCA      269
Phe Gly Ser Arg Xaa Glu Ser Thr Ser Pro Cys Thr Asp His Cys Ser
          5                      10                      15

GGA CCC AGA GAG GAG CAG CTC TGC TCC AGC AGG GTT TTC CAT TGC ATC      317
Gly Pro Arg Glu Glu Gln Leu Cys Ser Ser Arg Val Phe His Cys Ile
          20                      25                      30

ACA CAC CCA AAC GGT AGG ATC CAC CGG TGG                                347
Thr His Pro Asn Gly Arg Ile His Arg Trp
          35                      40

```

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 53..94
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SCVFFHFLQGGLG/FG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

AACTTTCTTC AAGGCGGTTT GGGATTGTC TCCGCTGGCC GCTGTGCTGG TG ATG TCC      58
                                         Met Ser

TGT GTT TTC TTT CAC TTT CTT CAA GGC GGT TTG GCA TTT GGC TCC GCT      106
Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly Ser Ala
          -10                      -5                      1

GGC CGC TGT GCT GGT GAC AGG                                127
Gly Arg Cys Ala Gly Asp Arg
          5                      10

```

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 156..215
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq LILLPIWINMAQI/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```

AAACTCGAAC TTGGTCGGGG CGCGGATCCC GAGAGGGAAA GTCATAACAA CCGCACCAGG   60
GAGTTCGACT GCGGAAGTGG AAGGCCACGC CTCCTCCGGC CTGCCCCCTC AGCCCTGTCC   120
CTGGGGGCAG AGCTCAGACT GTCTTCTGAA GATTG ATG TCT ATT TCC TTG AGC       173
                               Met Ser Ile Ser Leu Ser
                               -20                -15

TCT TTA ATT TTG TTG CCA ATT TGG ATA AAC ATG GCA CAA ATC CAG CAG       221
Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn Met Ala Gln Ile Gln Gln
          -10                -5                        1

GGA GGT CCA GAT GAA AAA GAA AAG ACT ACC GCA CTG AAA GAT TTA TTA       269
Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr Ala Leu Lys Asp Leu Leu
          5                10                15

TCT AGG ATA GAT TTG GAT GAA CTA ATG AAA AAA GAT GAA CCG CCA GGG       317
Ser Arg Ile Asp Leu Asp Glu Leu Met Lys Lys Asp Glu Pro Pro Gly
        20                25                30

```

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..151
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq SFCNAVVLSPVFO/EE

Lys Gly Glu Thr Cys Thr Glu Ile Glu Ser Val Tyr Leu Ala Pro Met
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

TACTGTGGTA AGCACTTAGT AATGCAAAGT ATTGTTATTC TAATTATTTC CAATAAGAAT 60
 AGTGCCTTTT ATTGGGGAAA GAGTCTACTT GGCTGATCAC AACAAGAGGT TTATTCTTTC 120
 CTCC ATG AGG TAC CGG TTA AGG ATT CAA ATC ACA ACA TCC CTC AAT CAG 169
 Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln
 -20 -15 -10
 ATC CTG CTA TTC TTA CTG ATA AGT TGT AGG ACC TTG AGC 208
 Ile Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser
 -5 1

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 201..345

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.2

seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```

ATGTAATGGA AGCAATCATT TTGAAAAGAG TTAAAGTTTT TTGTAAGTC AAATAAGGAT   60
CAATGCTGCT GAAAGCTGGG ACAACACACG GGCCCTGACC AAATTGGGGT TTCTTTGTCT  120
ACCTCATACC TTCCAAATCA AAAAATAATT TCCCTAGTAT TTTAATTACT CCCCCAAATC  180
AGGAATAACT TCCTCACTGT GCTGATTTTG GTTCTTTTAA AATAAGGTGG TAATTTGAAG  240
GTAATAGTTA AACCAGTCAT AGATTATTCT ATG CCA TTC TTT TCA AAT CAG CCC   294
                               Met Pro Phe Phe Ser Asn Gln Pro
                               -25                               -20

ACT CAG GTG TCA GTC CTA CTT TTC TTT TGT TGT AGT CCT CTT TAT TCT   342
Thr Gln Val Ser Val Leu Leu Phe Phe Cys Cys Ser Pro Leu Tyr Ser
      -15                      -10                      5

CCT TTG TTT CTG CTC CAV CTC ATC CCC CAC CAG   375
Pro Leu Phe Leu Leu Xaa Leu Ile Pro His Gln
      1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 32..163

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1

seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

GCTGCGGCCC GGCCGGCGG GTAAATAACA G ATG CGG GTG AAA GAT CCA ACT   52
                               Met Arg Val Lys Asp Pro Thr
                               -40

AAA GCT TTA CCT GAG AAA GCC AAA AGA AGT AAA AGG CCT ACT GTA CCT  100
Lys Ala Leu Pro Glu Lys Ala Lys Arg Ser Lys Arg Pro Thr Val Pro
      -35                      -30                      -25

```

| | |
|---|-----|
| CAT GAT GAA GAC TCT TCA GAT GAT ATT GCT GTA GGT TTA ACT TGC CAA His Asp Glu Asp Ser Ser Asp Asp Ile Ala Val Gly Leu Thr Cys Gln -20 -15 -10 | 148 |
| CAT GTA AGT CAT GCT ATC AGC GTG AAT CAT GTA AAG AGA GCA ATA GCT His Val Ser His Ala Ile Ser Val Asn His Val Lys Arg Ala Ile Ala -5 1 5 10 | 196 |
| GAG AAT CTG TGG TCA GTT TGC TCA GAA TGT TTA AAA GAA AGA AGA TTC Glu Asn Leu Trp Ser Val Cys Ser Glu Cys Leu Lys Glu Arg Arg Phe 15 20 25 | 244 |
| TAT GAT GGG CAG CTA GTA CTT ACT TCT GAT ATT TGG TTG TGC CTC AAG Tyr Asp Gly Gln Leu Val Leu Thr Ser Asp Ile Trp Leu Cys Leu Lys 30 35 40 | 292 |
| TGT GGC TTC CAG GGA TGT GGT AAA AAC TCA GAA AGC CAA CAT TCA TTG Cys Gly Phe Gln Gly Cys Gly Lys Asn Ser Glu Ser Gln His Ser Leu 45 50 55 | 340 |
| AAG CAC TTT AAG AGT TCC AGA ACA GAG CCC CTC AGG Lys His Phe Lys Ser Ser Arg Thr Glu Pro Leu Arg 60 65 70 | 376 |

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 9..140
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GTYLTSSSPLCQL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

| | |
|---|-----|
| ACTTTAAT ATG GTG TCC TTG GGT TAT TAT TTA ATA TTT GTC CTA TAT CTT Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu -40 -35 | 50 |
| TGG CTT TGT TTC ATG CAA ATT AGT GAA GAG AAG TTA ATA GAG GAA CAC Trp Leu Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His -30 -25 -20 -15 | 98 |
| ACA GGT ACA TAT TTA ACC TCC AGT TCA CCC CTC TGC CAG CTC CAG CCC Thr Gly Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro | 146 |

-10

-5

1

CCA GGG
Pro Gly

152

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq VLCCLLIATPTFF/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

ATATTATTAA ACTTTTATT TTGAGGTTAG TGTGGATTGA AATACTTC CAACAATTAA   60
CACAAAGGTC CCTGTGTCC TTTACCCAGT TTTCCACAAT GGTAACATCT TACAAAAC TG   120
GAGTACA ATG TCA CTC ACA TCC AGG RTA MYA ATW ATG GWT ACA ATC AAG   169
      Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys
      -35                      -30                      -25
ATA CAG AAT ATT TCT ATT ACA AAG GTC TTG TGT TGC CTT CTT ATA GCA   217
Ile Gln Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala
      -20                      -15                      -10
ACA CCT ACT TTC TTC CTA CTC CTT CCC TCA TCC ATT CCA CGG           259
Thr Pro Thr Phe Phe Leu Leu Leu Pro Ser Ser Ile Pro Arg
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 137..190
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq AGVVSTSVAAAVA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

AAGCGCAACC GGAAC TAGCC TTCTGGGGGC CGGCTTCCTT TATCTCTGGC GGCCTTGTAG   60
TCGTCTCCGA GACTCCCCAC CCCTCCTTCC CTCTTGACCC CCTAGGTTTG ATTGCCCTTT   120
CCCCGAAACA ACTATC ATG ARC GCC GAG GCT GCC GGT GTT GTC TCC ACC TCG   172
               Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser
               -15                               -10

GTG GCC GCG GCT GTT GCT GCT GTC GCT GCT CCT GCT GGG GCC GGG   217
Val Ala Ala Ala Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
   -5               1               5
  
```

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 101..145
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

TTGGTATCTG GAGTGTTGTA GTGTGTTTGT ATTTGCTTAT AAATAAGTAT TATAGATAAA   60
GATAAACTTC ATAAAGASTG GATATTTTGG GGAAATTTTC ATG TGG ATA ATG TCA   115
               Met Trp Ile Met Ser
               -15

TCC TGT CTG GCA TTG ACA TAC ACA AAT TCA ATC TCA CAT AGT CTT TGC   163
Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile Ser His Ser Leu Cys
-10               -5               1               5
  
```

CTT GAG AGA GCG TAC AGT CTA TTC AAA GTT GAC
 Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
 10 15

196

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 65..124
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

ACAGTGTGGC TCGGTTGAAT AGGAGAGCTT TAACTGCATT CTCTTGAG AATGCAGTBG 60
 AAGA ATG CCA AGA GGA GTG TAC AAT TCA AAT GCG TTA GTG CTT GTA ACA 109
 Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr
 -20 -15 -10
 CGT GGT TCC AGT TCT CTC CCT CTT GGC TTG TAT GGT ATA AAT TGT GTA 157
 Arg Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val
 -5 1 5 10
 CAG GTA ATT AAG TTA TTT TAT AGA GGC CAT CTC CAC TGG GAA ACT TTG 205
 Gln Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu
 15 20 25
 CTG CCA TCG 214
 Leu Pro Ser
 30

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 210..341
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FLLPCVHPFSVIA/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

```

AATTTATGAT AGGAAATGAT TGATCAAGTG TCACACAGCT GATTATCAGG TCTCAGTCTA   60
ATATTTATTC CTTATTGGTC TCTGCTTAAC TTCAAGTAGG TTATAGATTC CTTAATGGAC   120
TGATAGTTTA TGTCTTATAG CTTTACCTTT CAGGCGCTTA GTTTCATATT GGGAACATGA   180
CAAGTGAATA ATAAATACAT GATAGCTCT ATG ATT GAA CCC TGT GAG AAA ATG   233
                               Met Ile Glu Pro Cys Glu Lys Met
                               -40
AAG CAT TAT GAT ATG AAT TGG TTT CTG TGT ATG TAT GAG TGT TTT TTT   281
Lys His Tyr Asp Met Asn Trp Phe Leu Cys Met Tyr Glu Cys Phe Phe
-35                               -30                               -25
TTY CAT CTT TTG GAA ACA GAA TTT CTG CTC CCC TGT GTA CAC CCT TTC   329
Phe His Leu Leu Glu Thr Glu Phe Leu Leu Pro Cys Val His Pro Phe
-20                               -15                               -10                               -5
TCT GTA ATT GCA GTG TAT GTT TTT   353
Ser Val Ile Ala Val Tyr Val Phe
1

```

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 134..299
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq AALCC13LSQXFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```

AGCCTCCGCC TTTGCCTTCG CAGCCGCCTC CAGGGCAATT TGCATATTC TCCAAAGAAC   60
CATCCAGAAC CTGAGCAGCC TGTCTTCAGA CAGAGATAGG CCCACGGCTG TTTCTTGAAA  120
TCTGGCGCTG GGA ATG GCC ATG TGG AAC AGG CCA TGC CAG ARG CTG CCT   169
          Met Ala Met Trp Asn Arg Pro Cys Gln Xaa Leu Pro
          -55                    -50                    -45

CAG CAG CCT CTG GTA GCT GAG CCC ACT GCA GAG GGG GAG CCA CAC CTG   217
Gln Gln Pro Leu Val Ala Glu Pro Thr Ala Glu Gly Glu Pro His Leu
          -40                    -35                    -30

CCC ACG GGC CGG GAG CTG ACT GAG GCC AAC CGC TTC GCC TAT GCT GCC   265
Pro Thr Gly Arg Glu Leu Thr Glu Ala Asn Arg Phe Ala Tyr Ala Ala
          -25                    -20                    -15

CTC TGT GGC ATC TCC CTG TCC CAG TKA TTT CCT GAA CCG GGG           307
Leu Cys Gly Ile Ser Leu Ser Gln Xaa Phe Pro Glu Pro Gly
          -10                    -5                    1

```

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 130..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq CLLVSYAVDSAAG/RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

ATTGTCAAAA AGACATCAAA CTCAACTTCT GGGAAGACAG ATTTTAAATA CACATACTTG   60
GCTAATACTC ACAAACATAT CTAAAGTTTT GGCAAAATTA TGAGGGTGAT GGGTKGGTAC  120
TACCTGGC ATG GAG CAG GTG TGT CTT TTG GTT TCT TAT GCA GTT GAC TCT   171
          Met Glu Gln Val Cys Leu Leu Val Ser Tyr Ala Val Asp Ser
          -15                    -10                    -5

GCT GCA GGG AGA TTU GGG
Ala Ala Gly Arg Phe Gly
          1

```

189

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 20..103
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ATLRCWASTPVSG/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```

ACAAAGAGGC AGCTCCGGA ATG AGA AAG ATA AGC CAC TGC CTC CAC TGC TGG      52
      Met Arg Lys Ile Ser His Cys Leu His Cys Trp
                        -25                        -20

CCC GAG TCG GGG GCA ACA TTG AGG TGC TGG GCT TCA ACA CCC GTC AGC      100
Pro Glu Ser Gly Ala Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser
      -15                        -10                        -5

GGA AGG CTT TCC TCA ATG GCT GTK RWG SSG CKG GGG GAA AKG CCA CCA      148
Gly Arg Leu Ser Ser Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro
      1                        5                        10                        15

CAG GAT GCC TTC ACC ACA CAG TGG CTG GTG CGG GAC CTG AGG GGC AAG      196
Gln Asp Ala Phe Thr Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys
      20                        25                        30

ACT GAG AAG GAG TTT AAG GCC TAT GTG TCT TTG TTC ATG CGC CAT CTG      244
Thr Glu Lys Glu Phe Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu
      35                        40                        45

TGT GAG CCT GGG GCA GAC GGC TCT GAA ACC TTT GCC GAT GGG GTC CCT      292
Cys Glu Pro Gly Ala Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro
      50                        55                        60

CGG GAG GGA CTG AGT CGC CAG CAG GTG TTG ACC CGC ATT GGA GTC ATG      340
Arg Glu Gly Leu Ser Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met
      65                        70                        75

TCT CTC GTC AAA AAG AAG GGG CAG
Ser Leu Val Lys Lys Lys Gly Gln
      80                        85

```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 172..237
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLHPCGSITLTSS/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```

AAAATTTTT TAGCCTCTAA CATGAAAGGG TCTCTTCATT GTTCTCATTT GTCTTACCCG      60
CCATCCAGTG TTAAGCAGTA TGTTAAAGAG CTTCTTCTTT ACAACTTTTC CCCTCACATT      120
ATTTYCTAC ATGCAGCAAC TTCTTTAACC AAGTTGTTTG ATTAGGASTA A ATG TGC      177
                                     Met Cys
ATA AAC GAT CAT ATT ATT AAG CTT CTG CAC CCA TGT GGC AGC ATC ACT      225
Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser Ile Thr
-20          -15          -10          -5
TTA ACT TCT TCC TCA ACC ACA CGG      249
Leu Thr Ser Ser Ser Thr Thr Arg
1

```

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 135..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4
seq VALQCGLTIPALX/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```

AGAAGGGGTG TCAAACCTCA ATGGAAAAGG TTTAGGAAAA CACCTTTTAC AAATCCAAAG   60
ATGTTTCACA GTGGGCGAGG CTGGGTGTGGC GACAGTAGTG GCCACATGG CTGGGTTGGG   120
AGCCAGCTCT GCCC ATG AGG TGC CGT GTG GCT TTG CAG TGT GGC CTC ACA   170
          Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr
          -15 -10
ATC CCA GCT TTG TNT CTT CCC CAG GGA GAT GAG GCT GGT GAT GCT CAA   218
Ile Pro Ala Leu Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln
-5          1          5          10
GAT CTC AGA GGC CCT GCC CAG GCT GAG TAT CTG TAT ATA ATA TCC CCC   266
Asp Leu Arg Gly Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro
          15          20          25
TCG
Ser
269

```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 88..366
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LTS AFLWLPR LHI/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```

ATATACTCA GTTCTGTGTT GTCTTAGCT ACTGATGCAA ATGTGAAGAA TGAAAGTCTT   60
TCATCTGTGC ACCAGCTTGG CATTAAA ATG ACT GTC AGC TAT GGC AAA TTC CTC   114
          Met Thr Val Arg Tyr Gly Lys Phe Leu
          -90 -85
AGT CTC TTA AAA GAT GGT GCA GAA AAT GAT CTT ACC TGG GTT TTA AAG   162
Ser Leu Leu Lys Asp Gly Ala Glu Asn Asp Leu Thr Trp Val Leu Lys
          -80 -75 -70

```

| | |
|--|-----|
| CAT TGT GAG AGA TTC CTG AAA CAG CAG CAA ACT TCC ATA AAA TCT TCT His Cys Glu Arg Phe Leu Lys Gln Gln Gln Thr Ser Ile Lys Ser Ser -65 -60 -55 | 210 |
| CTT CTC TGC CTG CAA GGG AAT TAT GCT GGC CAT GAC TGG TTT GTA TCT Leu Leu Cys Leu Gln Gly Asn Tyr Ala Gly His Asp Trp Phe Val Ser -50 -45 -40 | 258 |
| TCT CTG TTC ATG ATA ATG TTG GGA GAC AAA GAA AAA ACA TTC CAA TTT Ser Leu Phe Met Ile Met Leu Gly Asp Lys Glu Lys Thr Phe Gln Phe -35 -30 -25 | 306 |
| CTT CAT CAA TTC TCC AGG CTT CTG ACT TCT GCT TTT CTT TGG TTG CCA Leu His Gln Phe Ser Arg Leu Leu Thr Ser Ala Phe Leu Trp Leu Pro -20 -15 -10 -5 | 354 |
| AGG CTA CAT ATT TCT GTA AGA CTT CAA TCT GTT TTT AAA GGA GGG TTT Arg Leu His Ile Ser Val Arg Leu Gln Ser Val Phe Lys Gly Gly Phe 1 5 10 | 402 |
| GAM ATT TTA AGA ACA TTA TAC TTA CAT TCA MCG GGA CGG Xaa Ile Leu Arg Thr Leu Tyr Leu His Ser Xaa Gly Arg 15 20 25 | 441 |

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..219
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFWVVLFSAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

| | |
|--|-----|
| ARCAGAGCCA CAGAATGCTG AGCAGTCAAC AGCATTCTT GTTCCAAGAT CACCCTTCTG | 60 |
| AGTACCTCTC TGGCTGCCAA ATTGCCAGGG CCTTCACAGT TTGATTCCAT TTCTCAGCTC | 120 |
| CAAGCATTAG GTRAAACCAC CAAGCAATCC TAGCCTGTG ATG GCG TTT GAC GTC Met Ala Phe Asp Val -20 | 174 |
| AGC TGC TTC TTT TGG GTG GTG CTG TTT TCT GCC GGC TGT AAA GTC ATC | 222 |

Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala Gly Cys Lys Val Ile
 -15 -10 -5 1

ACC TCC TGG GAT CAG ATG TGC ATT GAG AAA GAA GCC ACA 261
 Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu Ala Thr
 5 10

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 167..232
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq HLSSTTSPPWTHA/AT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAAACGCCT TGAGGATAAG GAAGGAGAAAT CAGCAAGTCC CGAGTTCCTA CGGTGTGTCA 60
 GCATCGTGCT CCCACTCCCG GGAGAGAGGC ATTATCTTCA GTTTACAAA GGGGAAAACA 120
 GGTCTGGGGT TTCCAGAGTC CGCGGTTTTG CTAAGAAGCC GCAGTG ATG TTG ACG 175
 Met Leu Thr
 -20
 CGG CTG GTC CTC AGT GCA CAC CTG AGT AGC ACG ACC TCT CCG CCC TGG 223
 Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser Pro Pro Trp
 -15 -10 -5
 ACG CAC GCT GCC ATC AGC TGG GAG CTG GAC AAC CTG CTG ATG CCT AGT 271
 Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu Met Pro Ser
 1 5 10
 CCC AGA ATC TGG CCC CTG 289
 Pro Arg Ile Trp Pro Leu
 15

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 326..445
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq CVNLLLGFEFVIS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```

ATAAACTTA GGGGAAGAT TTGCCTCTCA CTTTTTTTCT TGGAAAATGT GGGCAGCAAT   60
TTTAAAGAGA ACATGAAAT GGAGTAGGTT GAAACCAACA TTCAGAACTT CCTTTCATGG  120
ATTGAAACTT AAAGCTGAGG GAGGKTTTRA GGGTGGARKT RAGGAAGGGC TAGAAGATAG  180
CAAATTCAG AGTCATATCA GAGAATATGA ACTGTCACTG TTTCCAATGT TTCTCTTGGC  240
TCTGCACAGC ACTTCCAAGC CCTTTTGCTC ACTGTTTTCG TTCTGCCACA CCTAGGAGAA  300
GATTCAGAGC TTGCTGAGGC AAAAC ATG CGA TAT TTC CAA GGG CCT TCC CCC   352
                Met Arg Tyr Phe Gln Gly Pro Ser Pro
                -40                               -35

TAT TCT GAA ATA GAA ATT GAG CTT TGT GAT CAT GTG TAT TCA TTC CAA   400
Tyr Ser Glu Ile Glu Ile Glu Leu Cys Asp His Val Tyr Ser Phe Gln
   -30                -25                               -20

GGT CTA TCT GTT AAC CTT TTG CTA GGA TTT GAA CTT GTT ATT AGT AGG   448
Gly Leu Cys Val Asn Leu Leu Leu Gly Phe Glu Pro Val Ile Ser Arg
  -15                -10                               -5                               1

AGC CGR MGC AGT TCA CTT GCT GTT GAG TCT                               478
Ser Arg Met Ser Ser Leu Ala Val Glu Ser
      5                               10

```

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(iii) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 48..170
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LASLECYVPSTNQ/WQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```

ACTGCAGATA CGATCCCCGC TTCAACACCT GGATACACCT GGCCAGS ATG AAN HAG      56
                                     Met Xaa Xaa
                                     -40

AAG CGC ACG CAC TKV VNS STG AGC GTG TTC AAC GGG CTC GTG TAC GCC      104
Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu Val Tyr Ala
      -35                      -30                      -25

GCG GGC GGC CGC AAC GCA GAA GGA AGC CTG GCC TCG CTG GAG TGC TAC      152
Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu Glu Cys Tyr
      -20                      -15                      -10

GTG CCC TCC ACC AAT CAG TGG CAG CCG AAG HHN SDC CTG GAG GTG GCG      200
Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu Glu Val Ala
      -5                      1                      5                      10

CGC TGC TGC CAC GCT AGC GCG GTC GCC GAC GGC CGC GTG CTG GTG ACC      248
Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val Leu Val Thr
      15                      20                      25

GGA GGC TTG
Gly Gly Leu
                                     257

```

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 249..362
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LLFFHLLLNDEFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

ACATCCAGCT CTGGTAGTTT AGGCTCAATC TTACGGTGTA ATTATACAGA ATAATTAGAG 60
 GCAGCTGTAT CCTTGTTTCT GATTTTAAAA TCTGRATGTT TCTYCAATTC TTTGTGTA 120
 CTCCTTCAT TTGGTACATA TAGAAGTCTT CTTATGTGTT AATAAAGTCT TCTAAGATAG 180
 TATTCTGGTC ATTGGAGACA CCAAAAATCT ATGGGCACAG TCCTGTTCCT GTTCTTTTG 240
 CCAATAGA ATG TTC CTT AAG GTT CAG TCA CAG TCC TTT TAC DTC CCT TAC 290
 Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr
 -35 -30 -25
 AGA GAT TGT TTA AAT TTC CAC AAA AGC ACG TAT TTA CTC TTC TTT CAC 338
 Arg Asp Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His
 -20 -15 -10
 TTG TTA CTA AAT GAC TTC TTC ACA TTT TAC NTT GGT AAA 377
 Leu Leu Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 119..199
- (C) IDENTIFICATION METHOD: Von He: ne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIILIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

CAGAATGTTT TTTGCTGCCT CGCTTACATG GCAAACTCA CAAACCACCT ATACAATCCA 60
 AAAGAGGGGA AACAGCTCAT CTCATATTAA TTATGGTCCA TTTCBATGAT AGGATATT 118
 ATG CAA CCA TTA AAA ATC ATA TTT TAT CTG AGT GTT AGT ATA TGG ATT 166
 Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile
 -25 -20 -15
 ATT TTA ATT ATT TAT ACT TTT CAG TGT AAT TCT TCT CTG AGC ATA CTA 214
 Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu
 -10 -5 1 5
 CTT TTC GAG TTA 226
 Leu Leu Glu Leu

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..66
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RVAACCTAAAPLQA/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

AAGTGATGG ATG ATG AGA ACG ACA GCG AGA GTC GCT GCG TGT ACT GCT GCA 51
Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala
          -15                      -10

GCC CCA TTG CAA GCC CAC GGT GCA GRC ATT CAG CAG GRT CCA GAC AGS 99
Ala Pro Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa
-5              1              5              10

CTC TGS TCT RGA AGG CTC AGC AGA GRR GGR CTT TCT GCA GGG CGR CTG 147
Leu Xaa Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu
          15              20              25

CAC CCR AGC GAA ACA GAA GCT GAA CTG GAR GCC CCG GGT CGC GCG 192
His Gln Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala
          30              35              40

```

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

- (B) LOCATION: 140..241
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RWASSCLHPSARS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```

AASCCCAASG TGCTGCCGTT GCCCGTACAA CTCGGACTTG CTGTTGCTCG AGCCGCGTCT    60
GCACGGGTCT CGGACCGAGC GGAGTCCMAG CCTCGGTCCC GGAGCCCACC TTCGCCTCGC    120
CCTTGCCCAG CCTGCGGTG ATG GAG GCG GCC ACC ACA CTG CAC CCA GGC CCG    172
                Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro
                -30                                -25

CGC CCG GCG CTG CCC CTC GGG GCC CGG GCC CGC TGG GCG AGT TCC TGC    220
Arg Pro Ala Leu Pro Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys
                -20                                -15                                -10

CTC CAC CCG AGT GCC CGG TCT TCG AAC CCA GCT GGG AAG AGT TCG CGG    268
Leu His Pro Ser Ala Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg
                -5                                1                                5

ACC CCT
Thr Pro
10
  
```

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 92..178
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq LCPVIFFPNCWK/EY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```

AAGAAAGGAC ATTTTTTTTT TCTTGACTA ACTAGGCTGG ATTYCCAAA TTGTTTGAGT    60
GGGCGGTGCC CCTCTTAATG CTTCTGTAAG A ATG CAA GGT GTC AGG GGA CCT    112
                Met Gln Gly Val Arg Gly Pro
                -25

GTG TAC TTT TCC TGG AGC ACA ACC ATG TTG TGT CCT GTT ATA TTC TTT    160
  
```

Val Ser Phe Ser Trp Ser Thr Thr Met Leu Cys Pro Val Ile Phe Phe
 -20 -15 -10

CCA TCC AAC TGT TGG AAA GAA TAT AAC AGG ACA CAG 196
 Pro Ser Asn Cys Trp Lys Glu Tyr Asn Arg Thr Gln
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 177..230
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq FXLLFXFXFFRQ/XG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ACAAGTCTGT CCTCCCTAGG CTGGCAGCTC TGTCAGCACC CAGGTTGTTA GAATAGTTGT 60
 TAAACAGGT CATTCTGTTG CCAAGTAATT ACGGGGCCCT GSACTCAGTA ACCTTCCCCA 120
 CGAAGCAGGC CGTAGTGTGC TTACTGCTCT CCCTTGSCCT TCCATCCCCT ACTTTG ATG 179
 Met
 TNG GRR TTT TCT TTC YTT TTA CTT TTC YTT TAW TTT CYT TTT TTC CGC 227
 Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe Arg
 -15 -10 -5
 CAG KCT GGG 236
 Gln Xaa Gly
 1

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 359..427
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SVRLIFRFSVINA/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```

ACACTGTGAA ATGCAATTGT GCCTTGAATA AGAAGGTACC TAGAAGCCAA ATTAAAGTAA   60
TAATGACTTC TTATTGGCTT TGATTTTTCa TTGCAGTATA TGGGAATTGT ACAGCAGGAA  120
ATGCTTATCA TTAATTTCTG ATGTTTTTTA AAGCACAACCT CGAAACATTT CGATCAtACA  180
TACATAGCAG TAGAGATCTG TGCCCTTCAG GTACATTGWA TCTGACCATC AGTTTATATA  240
TGTCATTGAA TTTTAAGAAT ACTCATGTTA ATAATAGTCA TCTATCCTTG CATTTTGAAA  300
CTGTTCTAAT CITAGTGAAC TTGAATTGGA TTTCTGGGTA AAAGAATGTG TTTCTTTT   358
ATG TTG CTT CTG TCC GAA GCC TTG TCA GAA TCT GTC AGA CTC TTG TTT   406
Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe
      -20                      -15                      -10

AGG TTT AGT GTG ATC ATG GCG TCA GAG AAG CAA AGC TTT CAA ATA       451
Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile
      -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 319..369
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SLPCTTAFPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```

ATTCTTCTCT GGTTACCTCT ATCTACCCCC GAGTCAACAA GCCCTGCCTG ATTACGCAGC   60
AGCAGTTTCT CCTGGAGAGT ATATGCCCTT CCCTACCAGA GTGGCTGTGC TCTGTGGACC  120
AACGGCATTG GTGCCGTGGC TGGTGTTCCT ACCATTCCAG TGGGTTGGCT GCAGAGTTAT  180
CCTTTGTGGG TGGGAGAGAG CACCAGGCCT CAGGAATCTC CCTGCTGGTC CCAGCCTCCA  240
TCTCCTCCTC CCCAACCTG AACCTCTCCC GCAACCTGCA CCTCCCCCGA GAAGCCAGCC  300
ACAGAGGCAG AGAGCATC ATG GCT CTT ATC AGC CTG CCA TGC ACG ACA GCT   351
          Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala
                -15                      -10

TTC CCT TTA CTG TCC AGC AAG GTT TCC CAG CTT CTC TTG CCC CTC AGC   399
Phe Pro Leu Leu Ser Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser
   -5              1              5              10

```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 83..193
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```

AGTGGAGAGT CGAGCCTGGG GTCGGCGGAG ACWGCTGGTG TCTGAAGCCG CTCGCGCCCA   60
GGGTGACCCT GTTTGCAGCA CG ATG TCT GAA GAA GAG GCG GCT CAG ATC CCC   112
          Met Ser Glu Glu Glu Ala Ala Gln Ile Pro
                -35                      -30

AGA TCC AGT GTG TGG GAG CAG GAC CAG CAG AAC GTG GTG CAG CGT GTG   160
Arg Ser Ser Val Trp Glu Gln Asp Gln Gln Asn Val Val Gln Arg Val
   -25              -20              -15

GTG GCT CTG CCC CTG GTC AGG GCC ACG TGC ACC GCG GTC TGC GAT GTT   208
Val Ala Leu Pro Leu Val Arg Ala Thr Cys Thr Ala Val Cys Asp Val
   -10              -5              1              5

TAC AAT GCA GCC AAG GAC AGG CAC CCG CTG CTG GGC TCC GCC TGG   253
Iyr Ser Ala Ala Lys Asp Arg His Pro Leu Leu Gly Ser Ala Trp

```

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 8..223
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

AAAAAAG ATG GCG GCG GCG GCG GCA GCT GGT GCG GCC TCC GGG CTG CCG      49
      Met Ala Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro
                -70                      -65                      -60

GGT CCA GTG GCA CAA GGA TTA AAG GAA GCG TTA GTG GAT ACG CTC ACC      97
Gly Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr
                -55                      -50                      -45

GGG ATC CTA TCC CCA GTA CAG GAG GTG CGG GCG GCT GCT GAA GAA CAG     145
Gly Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln
                -40                      -35                      -30

ATT AAG GTG CTG GAG GTG ACG GAG GAA TTT GGT GTT CAC TTG GCA GAA     193
Ile Lys Val Leu Glu Val Thr Glu Phe Gly Val His Leu Ala Glu
                -25                      -20                      -15

CTG ACT GTA GAT CCC CAG GGG GCA CTG GCA ATC CGT CAG CTG GCA TCA     241
Leu Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser
-10                -5                1                5

GTC ATC TTG AAA CAA TAT GTG GAG ACT CAC TGG TGT GCC CAA TCA GAG     289
Val Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu
                10                15                20

AAA TTT AGG
Lys Phe Arg
... 25

```

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 114..464
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq XXXYLNFCPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

GTGAATTCGC CAGCGGGAGC GCGCTCGCGG WCCGCGCGTT CTCGCTTTC CCGGCTCCGT   60
CGCTGACGCG TCGTAGASTT GGSVWGCCGG AAGGCAACGG CAGCGGGATC GGG ATG   116
                                     Met
AAC AGC GGC GGC GGC TTC GGT TTG GGC TTA GGC TTC GGC CTC ACC CCC   164
Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu Thr Pro
-115                               -110                               -105

ACG TCG GTG ATT CAG GTG ACG AAT CTG TCG TCG GCG GTG ACC AGC GAG   212
Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr Ser Glu
-100                               -95                               -90                               -85

CAG ATG CGG ACG CTT TTT TCC TTC CTA GGA GAA ATC GAG GAG CTG CGG   260
Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu Leu Arg
-80                               -75                               -70

CTC TAC CCC CCG GAC AAC GCA CCT CTT GCT TTT TCC TCB DRA GTA TGT   308
Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Xaa Val Cys
-65                               -60                               -55

TAT GTT AAG TTT CGT GAT CCA TCA AGT GTT GGA GTG GCC CAG CAT CTA   356
Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln His Leu
-50                               -45                               -40

ACT AAC ACG GTT TTT ATT GAC AGA GST CTG RAT AST TGT TCC TTG TGC   404
Thr Asn Thr Val Phe Ile Asp Arg Xaa Leu Xaa Ser Cys Ser Leu Cys
-35                               -30                               -25

AGA AGG TTG GTA TCT CGC TTT KTT TGN HBT TAT TTG AAT TTC TGT CCT   452
Arg Arg Leu Val Ser Arg Phe Xaa Xaa Xaa Tyr Leu Asn Phe Cys Pro
-20                               -15                               -10                               -5

GTC TGT TAT TGC TTT AGC TTT CCT AGA GAT TGG CAA GTA GAC AGT ACT   500
Val Cys Tyr Cys Phe Ser Phe Pro Arg Asp Trp Gln Val Asp Ser Thr
1                               5                               10

CTC   503

```

Leu

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 47..85
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq MIEMLIFLOCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

ATTAACAAAG AGCAAGTTTA ACCTGAGTGG TCAACTTTTG CAGCAG ATG ATT GAR      55
                                   Met Ile Glu

ATG CTA ATA TTT CTA GAC TGT GTC CTG TCT TCC AAA GAT ACA ATA ACC      103
Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp Thr Ile Thr
-10          -5          1          5

ATG TTT GTG AAG TTC ATA CCT ATT TTT CCT TTT CCT TTG CAG TTT TAT      151
Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu Gln Phe Tyr
          10          15          20

TTC CCC TCT TTC CTT CTT TTG GAG      175
Leu Pro Ser Phe Leu Leu Leu Glu
          25          30

```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 49..285
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq VIGSLVLVLTMLTC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

ACATCACAAA AATTAGGTGA CCATGGTTAT GATAATTCTT TGCCTAGT ATG CAT CCA      57
                                     Met His Pro

TTT CTA GCT GCC CAC GGA CCT GCA TTT CAC AAA GGC TAC AAG CAT AGC      105
Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr Lys His Ser
-75                               -70                               -65

ACA ATT AAC ATT GTG GAT ATT TAT CCA ATG ATG TGC CAC ATC CTG GGA      153
Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His Ile Leu Gly
-60                               -55                               -50                               -45

TTA AAA CCA CAT CCC AAT AAT GGG ACC TTT GGT CAT ACT AAG TGC TTG      201
Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr Lys Cys Leu
                               -40                               -35                               -30

TTA GTT GAC CAG TGG TGC ATT AAT CTC CCA GAA GCC ATC GCG ATT GTT      249
Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile Ala Ile Val
                               -25                               -20                               -15

ATC GGT TCA CTC TTG GTG TTA ACC ATG CTA ACA TGC CGC CGG              291
Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg Arg
                               -10                               -5                               1
  
```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 33..74
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq IWPMASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

ATCTTAGTGT GACACATGAA CCCCTCCCCT TC ATG ATC TGG CCT ATG TCT GCC      53
                                     Met Ile Trp Pro Met Ser Ala
                                     -10
  
```

TCT GTA GCT ACT CTC TGG TCC TTT ACC TCT TAC ATA AGC TAC CCA AGC 101
Ser Val Ala Thr Leu Trp Ser Phe Thr Ser Tyr Ile Ser Tyr Pro Ser
-5 1 5

AGG TTT TAC TAT GAT GCT TGG 122
Arg Phe Tyr Tyr Asp Ala Trp
10 15

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 12..104
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LFIYLVFVECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

AAGGGTAATG G ATG GGA ATT GAT ATT TTC TAT CCT TCA CAC ATC CCA GAC 50
Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp
-30 -25 -20

TTT CAT CCT ATT CAT TTA TTC ATT TAT CTA GTG TTT GTA GAG TGC CTT 98
Phe His Pro Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu
-15 -10 -5

CTG TGT ACC AGG AAC TGR GAW AGK TTG TCC KGA TTC AAC TGT GAT AAC 146
Leu Cys Thr Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn
1 5 10

GCT CAA ATA ATC TTC ACA ACA GGC TCA TCC TCT AGT GGA GGA AAT AAA 194
Ala Gln Ile Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys
15 20 25 30

CCA TTT AAA AGT AGT TTA TGT ACA GTA CAT AGA GGC CAA GAA AGG GAA 242
Pro Phe Lys Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu
35 40 45

AGA ATA GAG TGC CAA GGG AAT GGG
Arg Ile Glu Cys Gln Gly Asn Gly
5C

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 24..284
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LILQASLKGELEA/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

AAATAGCTGA TTATGAACGT TTG ATG AAA GAA CTA AAT CAA AAG TTA ACT AAT   53
      Met Lys Glu Leu Asn Gln Lys Leu Thr Asn
      -85                               -80

AAA AAC AAC AAG ATA GAA GAT TTG GAG CAA GAA ATA AAA ATT CAA AAA   101
Lys Asn Asn Lys Ile Glu Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys
      -75                               -70                               -65

CAG AAA CAA GAA ACC CTA CAA GAA GAA ATA ACT TCA TTA CAG TCT TCA   149
Gln Lys Gln Glu Thr Leu Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser
      -60                               -55                               -50

GTA CAA GAA TAT GAA GAA AAA AAC WCC AAA ATC AAG CAA TTG CTT GTG   197
Val Gln Glu Tyr Glu Glu Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val
      -45                               -40                               -35                               -30

AAA ACC AAA AAG GAA CTG GCA GAT TCA AAG CAA GCA GAA ACT GAT CAC   245
Lys Thr Lys Lys Glu Leu Ala Asp Ser Lys Gln Ala Glu Thr Asp His
      -25                               -20                               -15

TTA ATA CTT CAA GCA TCT TTA AAA GGT GAG CTG GAG GCA AGC CAG CAG   293
Leu Ile Leu Gln Ala Ser Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln
      -10                               -5                               1

CAA GTA GAA GTC TAT AAA GTA AGG GTT TTA CTT TTT AAG ATT AAA AAA   341
Gln Val Glu Val Tyr Lys Val Arg Val Leu Leu Phe Lys Ile Lys Lys
      5                               10                               15

ATG TTT TTT CAT GTA GAA GTG AGG AAC GGG   371
Met Phe Phe His Val Glu Val Arg Asn Gly
      20                               25

```

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 33..371
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq RLLLCILIIVCYI/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```

ACAGTCCTAC CTTTGCTGAT GCCTACTCTA AT ATG GGA AAC ACT CTA AAG GAG      53
                               Met Gly Asn Thr Leu Lys Glu
                               -110

ATG CAG GAT GTT CAG GGA GCC TTG CAG TGT TAT ACG CGT GCC ATC CAA      101
Met Gln Asp Val Gln Gly Ala Leu Gln Cys Tyr Thr Arg Ala Ile Gln
-105                               -100                               -95

ATT AAT CCT GCA TTT GCA GAT GCA CAT AGC AAT CTG GCT TCC ATT CAT      149
Ile Asn Pro Ala Phe Ala Asp Ala His Ser Asn Leu Ala Ser Ile His
-90                               -85                               -80                               -75

AAG GAT TCA GGG AAT ATT CCA GAA GCC ATA GCT TCT TAC CGC ACG GCT      197
Lys Asp Ser Gly Asn Ile Pro Glu Ala Ile Ala Ser Tyr Arg Thr Ala
-70                               -65                               -60

CTG AAA CTT AAG CCT GAT TTT CCT GAT GCT TAT TGT AAC TTG GCT CAT      245
Leu Lys Leu Lys Pro Asp Phe Pro Asp Ala Tyr Cys Asn Leu Ala His
-55                               -50                               -45

TGC CTG CAG ATT GTC TGT GAT TGG ACA GAC TAT GAT GAG CGA ATG AAG      293
Cys Leu Gln Ile Val Cys Asp Trp Thr Asp Tyr Asp Glu Arg Met Lys
-40                               -35                               -30

AAG TTG GTC AGT ATT GTC GCT GAC CAG TTA GAG AAG AAT AGG TTG CTT      341
Lys Leu Val Ser Ile Val Ala Asp Gln Leu Glu Lys Asn Arg Leu Leu
-25                               -20                               -15

CTG TGC ATC CTC ATC ATA GTA TGC TAT ATC CTC TTT CTC ATG      383
Leu Cys Ile Leu Ile Ile Val Cys Tyr Ile Leu Phe Leu Met
-10                               -5                               1

```

(2) INFORMATION FOR SEQ ID NO: 203:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 92..208
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq VAYAIPSPISLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```

ACATGTTGAG TACTTTTTC TCACCTGTTT TTCCATTCCT GTTAGCCGGA GCAAAGGGC   60
CTCCAAGTCC TCTTTTAGAG AGAAATGACT A ATG CTC ATA CTA GCA GAT ACC   112
                               Met Leu Ile Leu Ala Asp Thr
                               -35
AGA CGT GTC CAA GGA GGT ACC TTG GGC TTA ATT CCA GCA GTT CTC AAC   160
Arg Arg Val Gln Gly Gly Thr Leu Gly Leu Ile Pro Ala Val Leu Asn
   -30               -25               -20
AGA GTC CAC GTG GCA TAT GCT ATA CCC AGC ATA CCT AGC CTC TTC TGC   208
Arg Val His Val Ala Tyr Ala Ile Pro Ser Ile Pro Ser Leu Phe Cys
   -15               -10               -5
CAG CGC TGG                               217
Gln Arg Trp
1

```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 343..402
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6

seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

```

CACACAATTA ATATTAATGG ATAAC TAATT GGAGTAATGA TTATTAGCTA CTGAATGCTG   60
ATAATAGAAG TCATATTTAA ATGCTTACTT AGTTACTTAA GTTAGTCAAG GACTCTGAAA   120
AAAATAAGGT TTAAAGTTAA CAGTGTCA TC AGTCATTCCC AGTTATCTTC TTATTTAAGA   180
ACAAGATGGT AATGCAGTTG CCTTTGTTTA TTAAATAGA AAAAATTAAA TCAGGATAAA   240
ATGACCCAAC TACAGTGATG TATTTGGACA CACTACTTCT TATCTTTCAA TATAGACTTT   300
TATTTCTGGA TTACCATAGA TGGAAATAGT ATTACTGGAC AT ATG TTG GTA GGT   354
                               Met Leu Val Gly
                               -20

ATT TAC TTC TGT GTT TTT CTT TTT CCC TTA ATT TCG AAT ACT TCT AGC   402
Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser Asn Thr Ser Ser
  -15                -10                -5

TAC AAA AAT TGT CAT AAA ACT TTG CAA CAC ACT ATA CCT CCC CAC GGG   450
Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile Pro Pro His Gly
  1                5                10                15

```

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..126
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLLQGACPCLI FL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```

ATG TTT CTC GCT CCC TCT CTG CTG ATC ACA AAG CTG CTG ACC GGG TCA   48
Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser
  -40                -35                -30

GAA AGT CCT GAT GGA AAT CCA CCA GCG CTG GGC AGG CCC CTC CTC CTC   96
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu
  -25                -20                -15

```



```

CAG GGA GCT TGT CCT TGC CTA ATT TTT CTT CGT CCT GAT GAG AAC AAA   144
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys
-10                      -5                      1                      5

AAA GAG GGG GRG GAG GAA AAG AAA AAC CAC AAA CTT CCT TTG AAA ACC   192
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr
          10                      15                      20

AGC TTA GGG                                                         201
Ser Leu Gly
          25

```

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 235..288
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SKSCLFYLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```

AAAGGTGGCT TCAGGACCAC CTCCTGAGAG CTCGTGTGTA TTTCATGTAT ATTCCCCAA   60
ATATATCAGC ATCTGACCCT TGGCTTCTGG GAGAAAGACA GAGGCGGAAC CCTGGCCGCC   120
CCAGAGAGAG GCAGCTGTGG GGGCAGAGAT GTAACAACCC TTTGAACCTT GACCTTGGAC   180
GCCAGGCTGT CCGGGAGCTT CTCCCACAAT GGCTGTTTTG GGGATGTGAC CTGG ATG   237
                                     Met
GAC CCA TCT GCT AGC AAA TCC TGT CTG TTT TAC CTC CAA AAA GTA TCT   285
Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val Ser
      -15                      -10                      -5

GGA ATT CCA GGG CTT CTC ACC                                         306
Gly Ile Pro Gly Leu Leu Thr
      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 207:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 54..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWLCLQAYLASFS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```

ACGTGTCCTC AGGATTTTCC TCTTGGGCTG GACAGTTTGC TCCCCTGGAG GGT ATG      56
                                         Met

AGC CTG ACT GCT AGT GGG CCA AGA GCT GCC TGG GAG GAA AGG GTG GGG      104
Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val Gly
-45                      -40                      -35                      -30

GGT CTC CAC ACT TGG GGT GCC AAC ATT CCT ACC GCC CCT GAT TCC CAG      152
Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser Gln
-25                      -20                      -15

CGG TGG CTC TGT CTT CAG GCG TAC CTG GCA TCC TTC AGT CTT GAG AGC      200
Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu Ser
-10                      -5                      1

CCC CAC AGA ATC TAC CTK GAA TCT CCT CCC ACG CTC CTT TTC CCC CCG      248
Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro Pro
5                      10                      15

CCG      251
Pro
20

```

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 117..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq AQLASFLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

ACCGCAGAAA ATGCTAGGTG CAAAGTTTGT CGAAAGAAAG GTSAGGATGA CAAATTGATC   60
TTGTGTGATG AGTGTAAATA AGCCTTYCCA CCTGTTTTGT CTGAGGCCGG CCCTCT ATG   119
                                         Met
AAG TAC CAG ATG GTG AGT GGC AGT GCC CAG CTT GCC AGC CCG CTA CTG   167
Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu Leu
  -20                      -15                      -10
CCA GGC GCA ACT CCC GTG GCA GGA ACT ATA CTG AAG AGT CTG CTT CTG   215
Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu Leu
  -5                      1                      5                      10
AGG ACA GTG AAG ATG ATG AGA GTG ATG   242
Arg Thr Val Lys Met Met Arg Val Met
      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 229..333
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq CFWGLMYXWLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

ACATCTGATC GATAATTATG TCACCTGTAC CTGTCGCCAG CTGTCTTGT TATGACGTTA   60
STTTTACTGC TAGAAATATC TAGTAGATGG CTGGAAATCT GCAGGCAAAG TGCAGAGGGA   120
GTGAGCCTGC GAGGAGAGGG SCTGGSCAAA GTSAMBGCCC TGGCCGCAG ACTTCTTATC   180

```

```

TAAAAAATGG.GAACAGTAGT GTCTTCCTAA AGGCACCATG GACTTAAA ATG AAT GGC      237
                                   Met Asn Gly
                                   -35

ACG TTT CCT GGG ACT TAT GTA TAT TTG GTT GCT TAT GGG GAC TTA CGT      285
Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly Asp Leu Arg
   -30                -25                -20

ATA TTT GGT TGC TTT TGG GGA CTT ATG TAT ATK TGG TTG CTT TTG GGG      333
Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu Leu Leu Gly
   -15                -10                -5

TCT NAA GGG                                          342
Ser Xaa Gly
1

```

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 66..157
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 216..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 152..218
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 220..279
id AA134726
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 64..103
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..40
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 98..130
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 34..66
 id AA134726
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 81..285
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..205
 id R17226
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 50..112
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 12.7
 seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```

GAGGCTGACT GTACGTTTCT TCTACTCTGG CACCACTCTC CAGGCTGCC ATG GGG CCC   58
                                   Met Gly Pro
                                   -20

AGC ACC CCT CTC CTC ATC TTG TTC CTT TTG TCA TGG TCG GGA CCC CTC   106
Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser Gly Pro Leu
      -15                      -10                      -5

CAA GGA CAG CAG CAC CAC CTT GTG GAG TAC ATG GAA CGC CGA CTA GCT   154
Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg Arg Leu Ala
      1                      5                      10

GCT TTA GAG GAA CGG CTG GCC CAG TGC CAG GAC CAG AGT AGT CGG CAT   202
Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser Ser Arg His
      15                      20                      25                      30

GCT GCT GAG CTG CGG AAC TTC AAG AAC AAG ATG CTG CCA CTG CTG GAG   250
Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro Leu Leu Glu
      35                      40                      45

GTG GCA GAG AAG GAG CGG GAG GCA CTC AGA ACT GAG GCC GRC ACC ATC   293
Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala Xaa Thr Ile
      50                      55                      60

TCN NVN GGA GTG GAT CGT CTG GAG CGG GAG GTA GAC TAT CTG         340
Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr Leu

```

75

| | |
|---|-----|
| AAAAATAGGAG TCTCTGGTAC TGCAAAACCCA CAGCCTGGAC TCAGAGCTCA AGTCTGAACT | 60 |
| CTACCTCCAG ACAGA ATG AAG TTC ATC TCG ACA TCT CTG CTT CTC ATG CTG | 111 |
| Met Lys Phe Ile Ser Thr Ser Leu Leu Leu Met Leu | |
| -20 -15 | |
| CTG GTC AGC AGC CTC TCT CCA GTC CAA GGT GTT CTG GAG GTC TAT TAC | 159 |
| Leu Val Ser Ser Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr | |
| -10 -5 1 5 | |
| ACA AGC TTG AGG TGT AGA TGT GTC CAA GAG AGC TCA GTC TTT ATC CCT | 207 |
| Thr Ser Leu Arg Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro | |
| 10 15 20 | |

```

AGA CGC TTC ATT GAT CGA ATT CAA ATC TTG CCC CGT GGG AAT GGT TGT    255
Arg Arg Phe Ile Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys
      25                      30                      35

CCA AGA AAA GAA ATC ATA GTC TGG AAG AAG AAC AAG TCA ATT GTG TGT    303
Pro Arg Lys Glu Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys
      40                      45                      50

GTG GAC CTC AAG CAT AGG                                           321
Val Asp Leu Lys His Arg
      55                      60

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..136
id T07474
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 16..156
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq VLELLAAVCLVRG/GH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

AGTTTACGTG CCATC ATG AAT TAT CAG TAT GGT TTC AAC ATG GTC ATG TCT    51
      Met Asn Tyr Gln Tyr Gly Phe Asn Met Val Met Ser
            -45                      -40

CAT CCA CAC GCT GTC AAT GAG ATT GCA CTA AGC CTG AAC AAC AAG AAT    99
His Pro His Ala Val Asn Glu Ile Ala Leu Ser Leu Asn Asn Lys Asn
-35                      -30                      -25                      -20

CCC AGA ACA AAA GCC CTT GTC TTA GAA CTG TTG GCA GCC GTT TGT CTT    147
Pro Arg Thr Lys Ala Leu Val Leu Glu Leu Leu Ala Ala Val Cys Leu
            -15                      -10                      -5

GTC AGA GGC GGG CAT GAA ATC ATT TTA TCA GCA TTT GAT AAC TTT AAA    195

```

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Arg | Gly | Gly | His | Glu | Ile | Ile | Leu | Ser | Ala | Phe | Asp | Asn | Phe | Lys | | |
| | | 1 | | | | | 5 | | | | | | 10 | | | | |
| GAG | GTT | TGT | GGA | GAA | AAA | CAG | CGC | TTT | GAG | AAG | TTG | ATG | GAA | CAT | TTC | 243 | |
| Glu | Val | Cys | Gly | Glu | Lys | Gln | Arg | Phe | Glu | Lys | Leu | Met | Glu | His | Phe | | |
| | 15 | | | | | 20 | | | | | 25 | | | | | | |
| AGG | AAT | GAA | GAC | AAT | AAC | ATA | GAT | TTT | ATG | GTG | GCT | TCT | ATG | CAG | TTT | 291 | |
| Arg | Asn | Glu | Asp | Asn | Asn | Ile | Asp | Phe | Met | Val | Ala | Ser | Met | Gln | Phe | | |
| | 30 | | | | 35 | | | | | 40 | | | | | 45 | | |
| ATT | AAT | ATT | GTA | GTC | CAT | TCA | GTA | GAA | GAT | ATG | AAT | TTC | AGA | GTT | CAC | 339 | |
| Ile | Asn | Ile | Val | Val | His | Ser | Val | Glu | Asp | Met | Asn | Phe | Arg | Val | His | | |
| | | | 50 | | | | | | 55 | | | | | 60 | | | |
| CTG | CAG | TAT | GAA | TTT | ACC | AAA | TTA | GGC | CTG | GMC | GAA | TAC | TTG | GRC | AAG | 387 | |
| Leu | Gln | Tyr | Glu | Phe | Thr | Lys | Leu | Gly | Leu | Xaa | Glu | Tyr | Leu | Xaa | Lys | | |
| | | 65 | | | | | | 70 | | | | | 75 | | | | |
| CTG | AAA | CAC | ACT | GAG | AGT | GAC | AAG | CTT | CAA | GTC | CAG | ATC | | | | 426 | |
| Leu | Lys | His | Thr | Glu | Ser | Asp | Lys | Leu | Gln | Val | Gln | Ile | | | | | |
| | | 80 | | | | | 85 | | | | | 90 | | | | | |

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..142
id HUM75321
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..142
id T08488
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 261..387

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..127
id R54273
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 205..288
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.7
seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
ATTGGAATT TTCAGCTCAC AAATGATGAA GAAATCCATA ACGTCGGAAC TTCCTTGACC   60
TTTGGATTG GCACATTGAC CTGCTGGATC CAGGCTGCGC TGACACTCAA GGTCAACATC  120
AASAATGAAG GACGGAGAGT TGAATTCCA CGGGTTATTC TGTCGGCATC TATCACTCTC  180
TGTGTGGTCC TCTACTTCAT CCTC ATG GCC CAA AGC ATC CAC ATG TAT GCA   231
                Met Ala Gln Ser Ile His Met Tyr Ala
                -25                               -20

GCC AGG GTC CAG TGG GGC CTG GTC ATG TGC TTC CTG TCT TAT TTT GGC   279
Ala Arg Val Gln Trp Gly Leu Val Met Cys Phe Leu Ser Tyr Phe Gly
                -15                               -10                               -5

ACC TTT GCC GTG GAG TTC CGG CAT TAC CGC TAT GAG ATT GTT TGC TCT   327
Thr Phe Ala Val Glu Phe Arg His Tyr Arg Tyr Glu Ile Val Cys Ser
                1                               5                               10

GAG TAC CAG GAG AAT TTC CTA AGC TTC TCA GAA AGC CTG TCA GAA GCT   375
Glu Tyr Gln Glu Asn Phe Leu Ser Phe Ser Glu Ser Leu Ser Glu Ala
                15                               20                               25

TCT GAA TAT CAG   387
Ser Glu Tyr Gln
30
```

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 124..335
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..212
 id AA081335
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 212..309
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..98
 id H88204
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 296..335
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 82..121
 id H88204
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 284..335
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..52
 id W31695
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 76..138
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LHLFHLIRPXQG/WX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```

ACTCTCTGCT GAACTCCCAA AGGGAGTGTG TGTATTTCTT CCGTCTCTN ATCAGAGCCC   60
CCAAAATAAG TAGGA ATG GGC AGT GGC TAT TCA CAT TCA CTA CAC CTT TTC   111
      Met Gly Ser Gly Tyr Ser His Ser Leu His Leu Phe
      -20                      -15                      -10

CAT TTG CTA ATA AGG CCC TGS CAA GGT TGG RAG GRA ATT GTC CCT GCC   159
His Leu Leu Ile Arg Pro Xaa Gln Gly Trp Xaa Xaa Ile Val Pro Ala
      -5                      1                      5

TGC TTC TGS AGA AAG AAG ATA TTG ACA CCA TCT ACG GGC ACC ATG GAA   207
Cys Phe Trp Arg Lys Lys Ile Leu Thr Pro Ser Thr Gly Thr Met Glu
      10                      15                      20

CTG CTT CAA GTG ACC ATT CTT TTT CTT CTG CCC AGT ATT TGC AGC AGT   255
Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser Ser
      25                      30                      35

```

AAC AGC ACA GGT GTT TTA GAG GCA GCT AAT AAT TTA CTT GTT GTT ACT 303
 Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr
 40 45 50 55

ACA ACA AAA CCA TCT ATA ACA ACA CCA AAC ACG TGG 339
 Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Trp
 60 65

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..116
id AA081350
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 277..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..50
id AA046671
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 157..204
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

AGGGAAATCC GGATGTCTCG GTTATGAAGT GGAGCAGTGA GGTGAGCCT CAACATAGTT 60
 CCAGAACTCT CCATCCGGAC TAGTTATTGA GCATCTGCCT CTCATATCAC CASTGGCCAT 120
 CTGAGGTGTT TCCCTGGCTC TGAAGGGGTA GGCACG ATG GCC AGG TGC TTC AGC 174
 Met Ala Arg Cys Phe Ser
 -15

(A) NAME/KEY: other

(B) LOCATION: 220..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 355..397
id N25870
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 20..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 143..299
id H99323
est

(ix) FEATURE:

[illegible]

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 67..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..196
id AA150024
est

(LX) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 171..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq MTCLSLVLFYGYS/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

| | |
|---|---------|
| AATCTTGTCA GAAGTCGTCG AAAATATTTA CACCAGCAGC TCCAGTTCAT ACCAATAAAG | 60 |
| AAGATCCTGC TACCCAAACT AATTTGGGRW TTATCCAWGC ATTTGKCGCT GCCATATCAG | 120 |
| TTATTAWT GK ATCYGAATTG GGTGATAAGA CATTTTTTAT AGCAGCCATC ATG GCA | 176 |
| | Met Ala |
| ATG CGC TAT AAC CGC CTG ACC GTG CTG GCT GGT GCA ATG CTT GCC TTG | 224 |
| Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu Ala Leu | |
| -30 -25 -20 | |
| GGA CTA ATG ACA TGC TTG TCA GTT TTG TTT GGC TAT GCC ACC AGT CAT | 272 |
| Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr Ser His | |
| -15 -10 -5 | |
| CCC CAG GGC CTA TAC ATA | 290 |
| Pro Gln Gly Leu Tyr Ile | |

TTC CCT GCC CCA TCC CCG TGC CCT TCT TGG CCT GTG GCG CTG GGG AGC 330
 Phe Pro Ala Pro Ser Pro Cys Pro Ser Trp Pro Val Ala Leu Gly Ser
 1 5 10

CAT GGT GTG GCA TAC TGG GGC TCC TGC TCC TTG GGS CAC 369
 His Gly Val Ala Tyr Trp Gly Ser Cys Ser Leu Gly His
 15 20 25

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 117..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..274
id C16636
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 121..360
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq RASLLPMLLGSWA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

AAAAAAGAGC TGGTTCCCTG GCAGGCTGGA GGGCAGGAGC TGGGCCACG CTGGTCTGGG 60

ATAGTTGGGC AGGGAGGCTG TCTACCTGGT CTTCCAGAAT GGACGGCCCT GTGGCAGAGC 120

ATG CCA AGC AGG AGC CCT TTC ACG TGG TCA CAC CTC TGT TGG AGA GCT 168
 Met Pro Ser Arg Ser Pro Phe Thr Trp Ser His Leu Cys Trp Arg Ala
 -80 -75 -70 -65

GGG CGC TGT CCC AGG TGG CGG GCA TGC CTG TCT TCC TCA AGT GTG AGA 216
 Gly Arg Cys Pro Arg Trp Arg Ala Cys Leu Ser Ser Ser Val Arg
 -60 -55 -50

ATG TGC AGC CCA GCG GCT CCT TCA AGA TTC GGG CCA TTG GGC ATN TCT 264
 Met Cys Ser Pro Ala Ala Pro Ser Arg Phe Gly Ala Leu Gly Xaa Ser
 -45 -40 -35

GCC AGG AGA TGG CCA AGA AGG GAT GCA GAC ACC TGG TGT GCT CCT CAG 312

Ala Arg Arg Trp Pro Arg Arg Asp Ala Asp Thr Trp Cys Ala Pro Gln
-30 -25 -20

GGG GTA ATG CGG GCA TCG CTG CTG CCT ATG CTG CTA GGA AGC TGG GCA 360
Gly Val Met Arg Ala Ser Leu Leu Pro Met Leu Leu Gly Ser Trp Ala
-15 -10 -5

TTC CTG CCA CCA TCG TGC TCC CCG AGA GCA 390
Phe Leu Pro Pro Ser Cys Ser Pro Arg Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 50..373
id AA147010
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..450
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 156..474
id AA142584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..450
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..229
id AA043641
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..304
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 72..275
id T18932

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 132..243
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 146..257
 id AA123074
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 165..284
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6
 seq LTYGIILTHGASG/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```

AACGCTGTGG CGGGGCAGGC GAGGCGGTGC CTCGAGCGC GCTAGTCAGC TCCCTGAAGG      60
GAGTGACGGC GGTGGGTGC CCGCGGCCAC TTTGCTTC CTGGGAGAT GTCCTTTGCT      120
TCTCAGATGT AAKGCACTT TAAGTTTGKW ATTCAACAGT GAAA ATG AGT CAT ACA      176
                                     Met Ser His Thr
                                     -40

GAG GTT AAA TTA AAA ATA CCT TTT GGA AAT AAA TTA CTA GAT GCT GTT      224
Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu Leu Asp Ala Val
-35                               -30                               -25

TGT TTG GTA CCT AAC AAG AGC TTA ACA TAT GGA ATA ATT CTT ACA CAT      272
Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile Ile Leu Thr His
-20                               -15                               -10                               -5

GGA GCA TCA GGA GAT ATG AAT CTT CCT CAT TTG ATG TCA CTG GCA TCC      320
Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met Ser Leu Ala Ser
                               1                               5                               10

CAT CTT GCA TCT CAT GGG TTT TTC TGC CTG AGA TTT ACC TGT AAA GGC      368
His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe Thr Cys Lys Gly
15                               20                               25

CTT AAT ATT GTA CAT AGA ATT AAG GCG TAT AAA TCA GTT TTG AAT TAC      416
Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser Val Leu Asn Tyr
30                               35                               40

CTG AAG ACA TCA GGM RAA TAC AAA CTT GCA GGT      449
Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly
45                               50                               55

```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 75..254
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 77
region 1..180
id T31666
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..126
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 88..141
id R58665
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 23..77
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 39..93
id R58665
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 157..231
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 63..137
id R14990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..50
id R14990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..254
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..120
id T26956

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 31..150
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LCXEFXSVASCD/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

AAAAAGGGGC GGTGCAGAGG CGGCAGGAAG ATG GAG TTG GGG AGT TGC CTG GAG      54
              Met Glu Leu Gly Ser Cys Leu Glu
              -40                      -35

GGC GGG AGG GAG GCG GCG GAG GAA GAG GGC GAG CCT GAG GTG AAA AAG      102
Gly Gly Arg Glu Ala Ala Glu Glu Glu Gly Glu Pro Glu Val Lys Lys
      -30                      -25                      -20

CGG CGA CTT CTG TGT STR GAG TTT RCC TCG GTC GCA AGC TGC GAT GCC      150
Arg Arg Leu Leu Cys Xaa Glu Phe Xaa Ser Val Ala Ser Cys Asp Ala
      -15                      -10                      -5

GCA GTG GCT CAG TGC TTC CTG GCC GAK AAC GAC TCG GAG ATG GAA AGG      198
Ala Val Ala Gln Cys Phe Leu Ala Xaa Asn Asp Trp Glu Met Glu Arg
      1                      5                      10                      15

GCT CTG AAC TCC TAC TTC GAG CCT CCG GTG GAG GAG AGC GCC TTG GAA      246
Ala Leu Asn Ser Tyr Phe Glu Pro Pro Val Glu Glu Ser Ala Leu Glu
              20                      25                      30

CGC CGA CCA DGG
Arg Arg Pro Xaa
      35

```

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 52..231
id AA099777
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 85..135
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..51
 id AA099777
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 138..222
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 83..167
 id HSB16C031
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 80..135
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 27..82
 id HSB16C031
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 145..314
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 43..212
 id AA068028
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 148..255
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.8
 seq AFVSGLLIGQCSS/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

AGGCAGTGAA TTGAGACCGG AGGGAATCTG GCCCCTAGAG GCTGGTACTT GGGCCCGAAA   60
CCCCCATCTC CGGCGGAGAG ACCGTCCGAG GTAATTGTCT GCCACGAGTG CACATTCTGA  120
AAACAGGRGR WTTTAAGKTT CCTAAAA ATG GGA AGA ACC TAC ATT GTA GAA GAG   174
           Met Gly Arg Thr Tyr Ile Val Glu Glu
           -35                               -30

ACT GTT GGC CAG TAT CTT TCA AAC ATA AAT CTC CAA GGA AAG GCT TTT   222
Thr Val Gly Gln Tyr Leu Ser Asn Ile Asn Leu Gln Gly Lys Ala Phe
      -25                               -20                               -15

ATC TCT GGC CTT TTA ATA GSA CAG TGT TCG TCA CAA AAG GAT TAT GTG   270
Val Ser Gly Leu Leu Ile Gly Gln Cys Ser Ser Gln Lys Asp Tyr Val

```

-10 -5 1 5 ..
ATT CTT GCC ACT AGA ACG CCA CCC AAA GAG GAG CAA AGT GAG AAC TTG 313
Ile Leu Ala Thr Arg Thr Pro Pro Lys Glu Glu Gln Ser Glu Asn Leu
 10 15 20

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..433
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..207
id R16604
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 432..474
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 207..249
id R16604
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..440
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..214
id N99558
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 109..171
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AGTATTTCAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCCCGTC TCCTCATGAA 60

TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTTCCTAAGC AGGGCAAA ATG GGG TCT 117
Met Gly Ser
-20

CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG ATT CCG CTT GCA CTT 165
Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro Leu Ala Leu
-15 -10 -5

TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT TTC CCG AAT GGG CAA ACT 213
Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn Gly Gln Thr
1 5 10

TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC GTG TGG TAT TTT GAA 261
Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp Tyr Phe Glu
15 20 25 30

GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA GTA ACA ACA GTT CTT 309
Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr Thr Val Leu
35 40 45

CTG GTA CTG GAG AAT AAT AAC AAC TAT AAA TGT TGC CAG AGT GAA AAC 357
Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln Ser Glu Asn
50 55 60

TGC AGC AAA AAA TAT GTG ACA CTG CTG TCA ATT ATC TTT TCT TCC CTC 405
Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe Ser Ser Leu
65 70 75

GGA ATT GCT TTT TCT GGA TAC TGC CTG GTC ATC TCT GCC TTG GGT CTT 453
Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala Leu Gly Leu
80 85 90

GTC CAA GGG CCA TAT TGC CGC 474
Val Gln Gly Pro Tyr Cys Arg
95 100

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..214
id N99558

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 399..459
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 278..338
 id N99558
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 359..407
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 237..285
 id N99558
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 128..334
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..207
 id R16604
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 333..386
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 207..260
 id R16604
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 10..72
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AAGGGCAAA ATG GGG TCT CGG AAG TGT GGA GGC TGC CTA AGT TGT TTG CTG   51
  Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu
    -20                -15                -10

ATT CCG CTT GCA CTT TGG AGT ATA ATC GTG AAC ATA TTA TTG TAT TTC   99
  Ile Pro Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe
    -5                1                5

CCG AAT GGG CAA ACT TCC TAT GCA TCC AGC AAT AAA CTC ACC AAC TAC   147
  Pro Asn Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr
    10                15                20                25

GTG TGG TAT TTT GAA GGA ATC TGT TTC TCA GGC ATC ATG ATG CTT ATA   195

```

```

Val Trp Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile
          30          35          40
GTA ACA ACA GTT CTT CTG GTA CTG GAG AAT AAT AAC AAC TAT AAA TGT      243
Val Thr Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys
          45          50          55
TGC CAG AGT GAA AAC TGC AGC AAA AAA TAT GTG ACA CTG CTG TCA ATT      291
Cys Gln Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile
          60          65          70
ATC TTT TCT TCC CTC GGA ATT GCT TTT TCT GGA TAC TGC CTG GTC ATC      339
Ile Phe Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile
          75          80          85
TCT GCC TTG GGT CTT GTC CAA GGG CCA TAT TGC CGC ACC CTT GAT GGC      387
Ser Ala Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg Thr Leu Asp Gly
          90          95          100          105
TGG GAG TAT GCT TTT GAA GGC ACT RCT GGA CGT TTC CTT ACA GAT TCT      435
Trp Glu Tyr Ala Phe Glu Gly Thr Xaa Gly Arg Phe Leu Thr Asp Ser
          110          115          120
AGC ATA TGG ATT CAG TGC CTG GAA      459
Ser Ile Trp Ile Gln Cys Leu Glu
          125

```

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 6..344
id H09880
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 408..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 355..401
id H09880
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 56..395
id H29351
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..432
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity
region 391..430
id H29351
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..369
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 41..345
id H94779
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..338
id N27248
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..278
id T74091
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 273..314
id T74091
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 346..408
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTSAAAT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```

ACTCCTTTTA GCATAGGGGC TTCGGCGCCA GCGGCCAGCG CAGTCGGTC TGGTAAGTGC   60
CTGATGCCGA GTTCCGTCTC TCGCGTCTTT TCCTGGTCCC AGGCAAAGCG GASGNAGATC  120
CTCAAACGGC CTAGTGCTTC GCGCTTCCGG AGAAAATCAG CGGTCTAATT AATTCCTCTG  180
GTTTGTTGAA GCAGTTACCA AGAATCTTCA ACCCTTTCCC ACAAAGCTA ATTGAGTACA  240
CGTTCCTGTT GAGTACACGT TCCTGTTGAT TTACAAAAGG TGCAGGTATG AGCAGGTCTG  300
AAGACTAACA TTTTGTGAAG TTGTAAAACA GAAAACCTGT TAGAA ATG TGG TGG TTT  357
                                   Met Trp Trp Phe
                                   -20

CAG CAA GGC CTC AGT TTC CTT CCT TCA GCC CTT GTA ATT TGG ACA TCT   405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
   -15                               -10                               -5

GCT GCT TTC ATA TTT TCA TAC ATT ACT GCA GTA ACA CTC CAC CAT ATA   453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
   1                               5                               10                               15

```

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 29..295
id AA041777
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..277
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..222
id HSC1QB111
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 135..281
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 56..202
 id H10738
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 81..133
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..53
 id H10738
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 75..277
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 6..208
 id HSC2KE111
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 89..263
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 2..176
 id W24981
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 106..228
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.4
 seq PLIFSLWC SGVLL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```

AAGAGTGC GC GGRSATTGGG GCTTTCCAGC TCTCACAGAA CTTTCAGCAT CCCCAGCTGC   60
CGGTCTTGGC ATCTTCGAAG TAAGGAGAGT TTTAGATGCT TCTGG ATG TTC AAT GCT   117
                                   Met Phe Asn Ala
                                   -40

AGC ACC TTT ACA GAC TGG AGC AGC TCG ATT TTC TTC GTA TTT ACT TTC   165
Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe Val Phe Thr Phe
-35                               -30                               -25

AAG AGC AAG AAA AGT GCT GGG CTC CCA CTT ATT TTC TCC CTG TGG TGT   213
Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe Ser Leu Trp Cys
-20                               -15                               -10

TCC GGA GTT CTG CTC CAT ATC CAC CAG AAA GCT GGC GGC CCA CGG CTT   261

```

282

(1x) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 219..328
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 62..171
 id AA114263
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 159..218
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..60
 id AA114263
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 222..308
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13.4
 seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```

GACTCTTACT GTTCTCATG GTGAGAAGAC AATATTTGCT TTCTCTTTT CCTTTCTTCC   60
GGATGAGAGG NTAAGCCATA ATAGAAAGAA TGGAGAATTA TTGATTGACC GTCTTTATTC  120
TGTGGGCTCT GATTCTCCAA TGGAATACC AAGGGATGGT TTCCATACT GGAACCCWWA  180
GGTAAAGACA CTCAAGGACA GACATTTTGT GCAGAGCATA G ATG AAA ATG GCA AGT  236
                                   Met Lys Met Ala Ser
                                   -25

TCC CTG GCT TTC CTT CTG CTC AAC TTT CAT GTC TCC CTC CTC TTG GTC   284
Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val Ser Leu Leu Leu Val
          -20                -15                -10

CAG CTG CTC ACT CCT TGC TCA GCT CAG TTT TCT GTG CTT GGA CCT CTG   332
Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser Val Leu Gly Pro Leu
          -5                1                5

```

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..411
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..230
 id C15003
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..411
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..230
 id HUM407E11B
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 182..369
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..188
 id C15677
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 212..369
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 26..183
 id HUM169E08B
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 274..399
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.2
 seq LLEDLVCFECQS/DD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```

ACCAGGAACA TCCAGCTATT TATGATAGCA TTTGCTTCAT TATGTCAAGT TCAACAAATG   60
TTGACTTGCT GGTGAAGGTG GGGGAGGTTG TGGACAGSCT CTTTGATTG GATGAGAAAC   120
TAATGTTAAG AATGGGTCAG AAATGGGGCT GCTCAGCCTC TGGACCAACC CCAGGAAGAG   180
TCTGAAGAGC AGCCAGTGTT TCGGCTTGTT CCCTGTATAC TCGAAGCTGC CAAACAAGTA   240
CGTTCTGAAA ATCCAGAATG GCTTGATGTT TAC ATG CAC ATT TTA CAA CTG CTT   294
                               Met His Ile Leu Gln Leu Leu
                               -40

ACT ACA GTG GAT GAT GGA ATT CAA GCA ATT GTA CAT TGT CCT GAC ACT   342
Thr Thr Val Asp Asp Gly Ile Gln Ala Ile Val His Cys Pro Asp Thr

```

| | | | | | | | |
|---|--|-----|--|-----|--|-----|-----|
| -35 | | -30 | | -25 | | -20 | |
| GGA AAA GAC ATT TGG AAT TTA CTT TTT GAC CTG GTC TGC CAT GAA TTC | | | | | | | 390 |
| Gly Lys Asp Ile Trp Asn Leu Leu Phe Asp Leu Val Cys His Glu Phe | | | | | | | |
| | | -15 | | -10 | | -5 | |
| TGC CAG TCT GAT GAT CCA GCC CGG | | | | | | | 414 |
| Cys Gln Ser Asp Asp Pro Ala Arg | | | | | | | |
| | | 1 | | 5 | | | |

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 66..96
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..31
id AA017304
esr

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: 114..242
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.2
 seq PMQLLQVLSDVLA/EI
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

|                                                                 |            |            |            |            |            |     |
|-----------------------------------------------------------------|------------|------------|------------|------------|------------|-----|
| AAACCGTTGC                                                      | CAAGGAGCTC | GACTCTGGGA | GCGGTCTAGA | GCCCCGGCGC | CTCCTGGGGG | 60  |
| GTGGGGAAAC                                                      | GGTTTCGTGA | GGAGAATTTC | AGTTAAAT   | ATAAGACCTA | ATT ATG    | 116 |
|                                                                 |            |            |            |            | Met        |     |
| AGT GAT CAA ATT AAA TTC ATT ATG GAC AGT CTC AAT AAG GAG CCC TTT |            |            |            |            |            | 164 |
| Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro Phe |            |            |            |            |            |     |
| -40                                                             |            | -35        |            | -30        |            |     |
| AGG AAG AAC TAT AAT TTA ATC ACG TTT GWT TCC TTT GAG CCA ATG CAA |            |            |            |            |            | 212 |
| Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met Gln |            |            |            |            |            |     |
| -25                                                             |            | -20        |            | -15        |            |     |
| CTA TTA CAA GTT CTC AGT GAT GTT CTG GCT GAG ATT GAC CCA AAG CAA |            |            |            |            |            | 260 |
| Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys Gln |            |            |            |            |            |     |

|                                                                 |    |    |   |     |
|-----------------------------------------------------------------|----|----|---|-----|
| -10                                                             | -5 | 1  | 5 |     |
| CTT GTG GAT ATC AGA GAG GAG ATG CCA GAG CAG ACA GCC AAA CGA ATG |    |    |   | 308 |
| Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg Met |    |    |   |     |
| 10                                                              | 15 | 20 |   |     |
| TTG AGC CTT CTT GGT ATT CTT AAG TAC AAA CCT TCA GGA AAT GCC ACA |    |    |   | 356 |
| Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala Thr |    |    |   |     |
| 25                                                              | 30 | 35 |   |     |
| GAT ATG AGT ACT TTT CGT CAG GGT TTG GTG ATT GGA AGT AAA CCT GTA |    |    |   | 404 |
| Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro Val |    |    |   |     |
| 40                                                              | 45 | 50 |   |     |
| ATT TAC CCA GTG CTC                                             |    |    |   | 419 |
| Ile Tyr Pro Val Leu                                             |    |    |   |     |
| 55                                                              |    |    |   |     |

## (2) INFORMATION FOR SEQ ID NO: 229:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..151  
id T34361  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..358
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 152..305  
id T34361  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 131..263  
id HSC16A051  
est



## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 74..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 1..130  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 340..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 267..300  
id HSC16A051  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 41..236  
id T35252  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 255..302
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 236..283  
id T35252  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 57..143  
id H92421  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 200..273  
id H92421  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity  
region 85..227

id T19059  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 205..270  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 228..293  
id T19059  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 93..329  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 4.6  
seq IIHAXGLVRECLA/XT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

```

AAGACCTGGG CGTCTGGAAT GATCTACGTG CTTAATAACA CCACTCGCCA CCATTTTCTC 60
CAGCTGGGAG TGTCCACTCG CCTTCCACCA GC ATG GCA AGG TCK TCA CAG KAC 113
 Met Ala Thr Ser Ser Gln Xaa
 -75

CGC CAG CTG CTC AGT GAC TAC GGG CCA CCG TCC CTA GGC TAC ACC CAG 161
Arg Gln Leu Leu Ser Asp Tyr Gly Pro Pro Ser Leu Gly Tyr Thr Gln
-70 -65 -60

GGA ACT GGG AAC AGC CAR RTG CCC CAA AGC AAA TAC GCG GAG CTG CTG 209
Gly Thr Gly Asn Ser Gln Xaa Pro Gln Ser Lys Tyr Ala Glu Leu Leu
-55 -50 -45

GCC ATC ATT GRA GAG CTG GGG AAG GAG ATC AGA CCC ATG TAC GCA GGG 257
Ala Ile Ile Xaa Glu Leu Gly Lys Glu Ile Arg Pro Met Tyr Ala Gly
-40 -35 -30 -25

AGC AAG AGT GCC ATG GAG AGG CTG AAG CGC GGC ATC ATT CAC GCT MSA 305
Ser Lys Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile His Ala Xaa
-20 -15 -10

GGN CTR GTT CGG GAG TGC TTG GCA GAM ACG GAA CGA ATG CCA GAT CCT 353
Gly Leu Val Arg Glu Cys Leu Ala Xaa Thr Glu Arg Met Pro Asp Pro
-5 1 5

AGC TGC CTT GTT GGT TTT 371
Ser Cys Leu Val Gly Phe
10

```

## (2) INFORMATION FOR SEQ ID NO: 230:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 107..234
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..128  
id N88564  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 59..103
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5  
seq LLGAAVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```
AACCGGCAGC TGAACCCACC CGGCGCCACG GGACTTTGAC GCGTGCTCTG CGCTTGCC 58
ATG AGA CTC CTG GGA GCT GCA GCC GTC GCG GCT CTG GGG CGC GGA AGG 106
Met Arg Leu Leu Gly Ala Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
-15 -10 -5 1
GCC CCC GCC TCC CTA GGC TGG CAG AGG AAG CAG GTT AAT TGG AAG GCC 154
Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
 5 10 15
TGC CGA TGG TCT TCA TCA GGG GTG ATT CCT AAT GAA AAA ATA CGA AAT 202
Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
 20 25 30
ATT GGA ATC TCA GCT CAC ATT GAT TCT GGG AAG 235
Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys
 35 40
```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 13..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 20..169  
                           id N41898  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 26..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 38..174  
                           id H69272  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 45..162  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 1..118  
                           id N20619  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 13..60  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 4.5  
                           seq RLLRRFLASVIS/RK

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

```

AATTGCAGGG AG ATG GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT 51
 Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser
 -15 -10 -5

GTC ATC TCC AGG AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC 99
Val Ile Ser Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser
 1 5 10

AGA GCC CTG CAG ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA 147
Arg Ala Leu Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr
 15 20 25

CCC AAC CCA GCG CCG GGG 165
Pro Asn Pro Ala Pro Gly
 30 35

```

## (2) INFORMATION FOR SEQ ID NO: 232:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs  
 (B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 59..214  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..156  
id AA069390  
est

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 122..169  
(C) IDENTIFICATION METHOD: Von Haefne matrix  
(D) OTHER INFORMATION: score 4.4  
seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```

AAGGAGAGTC ACGTGAGAST GGGCGGAGGG GGTGGAGGTT TGTCTCCGCT GTTTCATCTC 60
TATGGCTGTC AGAGSTGGGC GGCTTTGACC GAGAGGCTGC TGCAGCTCGT GTTTGGACGC 120
G ATG TTT CGT CTG AAC TCA CTT TCT GCT TTG GCA GAA CTG GCT GTG GGT 169
Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
 -15 -10 -5

TCT CGA TGG TAC CAT GGA GGA TCA CAG CCC ATC CAG ATC CGG CTA GCC 217
Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
 1 5 10 15

```

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 358 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Muscle

(ix) FEATURE:  
(A) NAME/KEY: other  
(B) LOCATION: 44..169  
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100  
region 1..126  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 170..231  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 126..187  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 230..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 185..216  
id AA094226  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 129..280  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 193..254  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 279..340  
id R13710  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..282  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 172..410  
id R54574  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..184  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 159..299  
id T78111  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 182..222  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 298..338  
                           id T78111  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 220..254  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 337..371  
                           id T78111  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 89..271  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 3.9  
                           seq YTAHSVLAGPRWA/DP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

GCGGCGCGGC CGTAAAGCGC CATTACGCAG AGAGAAAGTT AAGAGAAACT CGTTTTCATC 60
TTCTTGTTTT CATCTTAATA CCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA 112
 Met Ser Gly Ser Asn Gly Ser Lys
 -60 -55

GAA AAT TCT CAC AAT AAG GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA 160
Glu Asn Ser His Asn Lys Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys
 -50 -45 -40

GTT GAA CGA AGC CAG GTT CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG 208
Val Glu Arg Ser Gln Val Pro Asn Glu Lys Val Gly Trp Leu Val Glu
 -35 -30 -25

TGG CAA GAC TAT AAG CCT GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT 256
Trp Gln Asp Tyr Lys Pro Val Glu Tyr Thr Ala Val Ser Val Leu Ala
 -20 -15 -10

GGA CCC AGG TGG GCA GAT CCT CAG ATC AGT GAA AGT AAT TTT TCT CCC 304
Gly Pro Arg Trp Ala Asp Pro Gln Ile Ser Glu Ser Asn Phe Ser Pro
 -5 1 5 10

AAG TTT AAC GAA AAG GAT GGG CAT GTT GAG AGA AAG AGC AAG AAT GGC 352
Lys Phe Asn Glu Lys Asp Gly His Val Glu Arg Lys Ser Lys Asn Gly
 15 20 25

CTG TAT
Leu Tyr

```

## (2) INFORMATION FOR SEQ ID NO: 234:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 base pairs

(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 294..347  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 297..350  
id AA038489  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 134..347  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..214  
id AA111922  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 284..331  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 3.5  
seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```
AAAAAAAGC TGCTGGACCC CAGGGAGAGC TGACCACTGC CCGAGCAGCC GGCTGAATCC 60
ACCTCCACAA TCGSGCTCTC AGGAACCCCG GYCCCTAATA ABAAGAGGAA ATCCAGCAAG 120
CTGATCATGG AACTCACTGG AGGTGGACAG GAGAGCTCAG GCTTGAACCT GGGCAAAAAG 180
ATCAGTGTCC CAAGGGATGT GATGTTGGAG GAACTGTCGC TGCTTACCPA CCGGGGCTCC 240
AAGATGTTCA AACTGSGGCA GATGAGGGTG GAGAAGTTA TTT ATG AGA ACC ACC 295
 Met Arg Thr Thr
 -15

CTG ATG TTT TCT CTG ACA GCT CAA TGG WTC ACT TCC AGA AGT TCC TTC 343
Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser Arg Ser Ser Phe
 -10 -5 1

CAA 346
Gln
5
```

(2) INFORMATION FOR SEQ ID NO: 235:



- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 384 base pairs  
    (B) TYPE: NUCLEIC ACID  
    (C) STRANDEDNESS: DOUBLE  
    (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Homo Sapiens  
    (D) DEVELOPMENTAL STAGE: Fetal  
    (F) TISSUE TYPE: kidney
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 35..384  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 93  
                            region 8..357  
                            id H11129  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 43..346  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 16..319  
                            id R11829  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 50..302  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 99  
                            region 1..253  
                            id R18811  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 302..366  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 254..318  
                            id R18811  
                            est
- (ix) FEATURE:  
    (A) NAME/KEY: other  
    (B) LOCATION: 183..371  
    (C) IDENTIFICATION METHOD: blastn  
    (D) OTHER INFORMATION: identity 96  
                            region 6..194  
                            id R10511  
                            est
- (ix) FEATURE:  
    A) NAME/KEY: sig\_peptide

(B) LOCATION: 73..147  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 14.1  
 seq LLLLLLTLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```

ACTGCGCGGA TCGGCGTCCG CAGCGGGCGG CTGCTGAGCT GCCTTGAGGT GCAGTGTG 60
GGATCCAGAG CC ATG TCG GAC CTG CTA CTA CTG GGC CTG ATT GGG GGC CTG 111
 Met Ser Asp Leu Leu Leu Leu Gly Leu Ile Gly Gly Leu
 -25 -20 -15

ACT CTC TTA CTG CTG CTG ACG CTG CTG GCC TTT GCC GGG TAC TCA GGG 159
Thr Leu Leu Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly
 -10 -5 1

CTA CTG GCT GGG GTG GAA GTG AGT GCT GGG TCA CCC CCC ATC CGC AAC 207
Leu Leu Ala Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn
 5 10 15 20

GTC ACT GTG GCC TAC AAG TTC CAC ATG GGG CTC TAT GGT GAG ACT GGG 255
Val Thr Val Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly
 25 30 35

CGG CTT TTC ACT GAG AGC TGC AGC ATC TCT CCC AAG CTC CGC TCC ATC 303
Arg Leu Phe Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile
 40 45 50

GCT GTC TAC TAT GAC AAC CCC CAC ATG GTG CCC CCT GAT AAG TGC CGA 351
Ala Val Tyr Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg
 55 60 65

TGT GCC GTG GGC AGC ATC CTG AGT GAA GGT GAG 384
Cys Ala Val Gly Ser Ile Leu Ser Glu Gly Glu
 70 75

```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 75..213  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
 region 29..172  
 id T64530

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 36..131
- (C) IDENTIFICATION METHOD: Von Helms matrix
- (D) OTHER INFORMATION: score 11.4  
seq LWSLALWLPLALS/VS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```

AATCCGGACT GATAACCAGC CGGCCAGACT GAGGG ATG GAA GGC ACT GAG ATG 53
 Met Glu Gly Thr Glu Met
 -30

GGG GCC CGT CCA GGC GGA CAC CCG CRG AAA TGG AGC TTT CTG TGG TCT 101
Gly Ala Arg Pro Gly Gly His Pro Xaa Lys Trp Ser Phe Leu Trp Ser
-25 -20 -15

CTT GCA CTC TGG CTG CCT CTT GCC CTC TCT GTG TCT CTC TTT CTT GGT 149
Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser Val Ser Leu Phe Leu Gly
-10 -5 1 5

CTC TCC CTC TCT CCT CCT CAG CCT GGT CTT TCT CTT TGG TGC ACA CTT 197
Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu Ser Leu Trp Cys Thr Leu
10 15 20

AGT TAT TGT TGT GAG CAA TGG AAG TTC AAA GGA ACT CCC TCT CCA GCT 245
Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys Gly Thr Pro Ser Pro Ala
25 30 35

CTT CTG AAT CTK GGG ACA CGC GGG 269
Leu Leu Asn Leu Gly Thr Arg Gly
40 45

```

## (2) INFORMATION FOR SEQ ID NO: 237:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 207..383  
id N28787  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 95..194  
id N28787  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 220..316  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 209..305  
id AA019783  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 97..196  
id AA019783  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 307..392  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 297..382  
id AA019783  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 108..207  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 99..198  
id H86396  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 307..374  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 300..367  
id H86396  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 255..313  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 247..305

id H86396  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 210..326  
id H86516  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 98..197  
id H86516  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 327..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 318..359  
id H86516  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 111..210  
id AA059290  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 272..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 285..367  
id AA059290  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91  
region 223..289  
id AA059290  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 133..302
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.2  
seq LLFALGSLGLIFA/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

ARCGGTTAGT GGACCGGGAC CGGTAVGGGT GCTGTWGCCA TCATGGCTGA CCCCMMCCC 60
CGGBACMCTC GCTCCTCGAT CGAGGACGAC TTCANMTMNG GCAGGCAAGC GTGGCCTCCG 120
CCACCGTGYM BNTCCGA ATG VCC TTT CTG ACA AAA GTT TMN AGC ATT CTT 170
 Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu
 -55 -50 -45

TCT CTG CAG GTT CTC TTA ACT ACA GTG ACT TCA ACA GTT TTT TTA TAC 218
Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr
 -40 -35 -30

TTT GAG TCT GTA CGG ACA TTT GTA CMT GAG AGT CCT GCC TTA ATT TTG 266
Phe Glu Ser Val Arg Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu
 -25 -20 -15

CTG TTT GCC CTC GGA TCT CTG GGT TTG ATT TTT GCG TTG ATT TTA AAC 314
Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn
 -10 -5 1

AGV CAT AAG TAT CCC CTT AAC CTG TAC CTA CTT TTT GGA TTT ACG CTG 362
Xaa His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu
 5 10 15 20

TTG GMA GCT CTG ACT GTG GCA GTT GTT GTT ACT 395
Leu Xaa Ala Leu Thr Val Ala Val Val Val Thr
 25 30

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..155
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 24..126  
id AA075942  
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 66..136  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 37..107  
                           id AA262924  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 22..135  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 10.8  
                           seq MLLLLLLLGSQG/PQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```

AAAGGGTCGT TGGTGGGAAA G ATG GCG GCG ACT CTG GGA CCC CTT GGG TCG 51
 Met Ala Ala Thr Leu Gly Pro Leu Gly Ser
 -35 -30

TGG CAG CAG TGG CGG CGA TGT TTG TCG GCT CGG GAT GGG TCC AGC ATG 99
Trp Gln Gln Trp Arg Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met
-25 -20 -15

TTA CTC CTT CTT CTT TTG TTG GGG TCT GGG CAG GGG CCA CAG CAA GTC 147
Leu Leu Leu Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val
-10 -5 1

GGG GCG GGG 156
Gly Ala Gly
5

```

## (2) INFORMATION FOR SEQ ID NO: 239:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(64..95)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 79..110  
                           id N98118  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 195..317  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.9  
 seq ILPFLLEFPFVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```

ATAGTGATCC TTTTCCTTCT CCCACTCCGT AAGTTTCTAT CCTTGGCCTC CTATTCTTTT 60
TACTACATAT ATACTTTATA TATACATATA TACTTGAAC AGGCTTAATG AGTTCCAAGG 120
TTTCAAGTAT AATAGAAGGA TAGTTTCCCT AATATTTCTT CAAAACAGAT TTCTCTTCTG 180
AAATCCAGAG TCAT ATG TCC AGT TGG ATG TAT CTT GGA TAC CCC ATT GTC 230
 Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val
 -40 -35 -30
ACC TCA AAC ACT ACT TGT CTA AAA CTG ATC TCA TCA TCT TTT CCC CAA 278
Thr Ser Asn Thr Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln
 -25 -20 -15
ATC CTT CCT TTT CTT CTA TTT CCC TTC CCA GTG AAT GCC AGA TCT CAC 326
Ile Leu Pro Phe Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His
 -10 -5 1
TYA GTT GCT CAA ACT AAA AGC CCG AGG 353
Xaa Val Ala Gln Thr Lys Ser Pro Arg
 5 10

```

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (E) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 88..132  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
 region 352..396  
 id AA021024  
 est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 46..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.7  
 seq QLCLLLLPSCSLV/VS



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```
ACCTCTTGGG GCCTACTTTG GGATGAAGTR GCCTCCCTCA GCAGC ATG GCC CCT GGG 57
 Met Ala Pro Gly
 -20

GTC ATC ATC ATC CAG CTC TGC CTC TTG CTC CTG CCT TCC TGC TCC CTT 105
Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Leu Pro Ser Cys Ser Leu
 -15 -10 -5

TCT GTT TCC GGA TGT TCC TGC CCT AGT GCC TGC TTC AGC ACC ACC AGC 153
Ser Val Ser Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe Ser Thr Thr Ser
 1 5 10 15

CGC GAG 159
Arg Glu
```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 80  
region 179..213  
id N73639  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 193..232  
id AA150411  
est

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 99..377
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.6  
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```

ACATGCTCAG GGTCAAGTTC CAGCCCCAGC TGAGGGCTGA GGGGAGTGGG TGGACATGGG 60
GCAGGGAGCT GGAAGAACAC TCGAGAGACA GCAGGTAG ATG AGA CAT GGC TTT ATT 116
 Met Arg His Gly Phe Ile
 -90

CAG CAG CAG TTT TCA TTA ACA GCT TTC TCA MAC STT WRG SCW ATC TTC 164
Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser Xaa Xaa Xaa Xaa Ile Phe
 -85 -80 -75

ACA CTG KST GSC CTG TCT CAG TTG CTT AGT TCA GCA GCT CCC AAA CAC 212
Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser Ser Ala Ala Pro Lys His
 -70 -65 -60

ACA GCT GCA CCG ACG GCC CTC CCT TGC CTT CAG GGT CAG CAG CTT AAC 260
Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu Gln Gly Gln Gln Leu Asn
 -55 -50 -45 -40

TCT CTC TCT CTG GGC ACA AGT GAG CTG AGC TGT GTC CTG GCT TCC TCC 308
Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser Cys Val Leu Ala Ser Ser
 -35 -30 -25

TGT CTA TCT ACA AAG ACA GAC CCC TCT GGT CTC TCT CTC TCT TTG GGT 356
Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly Leu Ser Leu Ser Leu Gly
 -20 -15 -10

GCC AGC GCA CCT GTA CAG TGT CAG CAG GAC AAT TAT ACC TTT TGC KNN 404
Ala Ser Ala Pro Val Gln Cys Gln Gln Asp Asn Tyr Thr Phe Cys Xaa
 -5 1 5

CAA TAC TGG CTT AGA GCA AGG CAT 428
Gln Tyr Trp Leu Arg Ala Arg His
 10 15

```

(2) INFORMATION FOR SEQ ID NO: 242:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 325..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 277..323  
id AA015580

est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 325..371  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 277..323  
 id AA019963  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 140..262  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.5  
 seq LIIFLSFLPFINS/SF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```

ACAAGTGGGA TAGGTCCTGT GACAGAATTG TGTGATACAG GTCAAACAGG AGTTGGGTTA 60
TGGGGAAAAT GCCAGTTGAA ATATGTTTTG ATCTTTGGAG AAACCTATTT TTTCATTTAA 120
CCTGTTCTTT AAATCCAGT ATG TTC CAG AAC ATA CAA AAA TGT TTA AAT GTT 172
 Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val
 -40 -35

CCA TTT GTA AGA GGA TAT CAT GTA TTT TAT ATC AAT TTA AAT GCA GTT 220
Pro Phe Val Arg Gly Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val
-30 -25 -20 -15

ATC CTA ATC ATT TTT CTT TCA TTT TTA CCC TTT ATT AAC TCT TCA TTT 268
Ile Leu Ile Ile Phe Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe
 -10 -5 1

GTT TAC AAA ACA AAT CCA CTC TAT GAC GCA ATC TCT AAT TAT GTG TTT 316
Val Tyr Lys Lys Thr Asn Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe
 5 10 15

TCT TTC AGG TAT CCA AAC CTT GRA ASC TTT GCT CTA GAT GTC AGG CTT 364
Ser Phe Arg Tyr Pro Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu
 20 25 30

GTT TTT 370
Val Phe
35

```

## (2) INFORMATION FOR SEQ ID NO: 243:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: cDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(215..358)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 165..308  
id R98055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 185..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 252..356  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..186
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 202..252  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 139..175  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 315..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 385..422  
id W23510  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(215..358)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 144..287  
id T46976  
est

## (ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(227..358)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 167..298  
                           id AA084768  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(248..358)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 169..279  
                           id R50108  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(215..250)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 94  
                           region 278 313  
                           id R50108  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 281..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 9.2  
                           seq FPVLAFLSGSLA/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```

AGAGTGAGAC GGGCAGATGG AGGAGGGATT GTAATGGCGG YAGCGGCAGC TCCSTGCTC 60
TGACCCACGG CAGGCATACA GCATCCGATT TAATCTGGAT CCATTCCGGC GCCTTCCTCT 120
CCCAGTCACC CAGAGGGCCC CAACCCCGGC GGCCTTTCT TCCTCAAATC TCCTCGGCTC 180
TATACCGTGC CTGGGTCTTT TCTCTTTCTC TCTGCCTGGA AGATTCCTTC TTTCCCCTTT 240
TGTCTTGCCC ACTCCTGTTT ACCCTTCAAG TTTCAAGTTC ATG TCA CTG TCT CAG 295
 Met Ser Leu Ser Gln
 -20
AGA GGT TTT CCT GTG CTC GCC CTG TTT CTC TCA GGA AGC CTT GCT CTT 343
Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser Gly Ser Leu Ala Leu
-15 -10 -5 1
TTC CAT CAT ACC TCT GGG
Phe His His Thr Ser Gly
 5

```

## (2) INFORMATION FOR SEQ ID NO: 244:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 base pairs

(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..132  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..114  
id N87112  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 194..267  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity ..  
region 174..247  
id N87112  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 130..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 111..176  
id N87112  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 68..267  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 1..200  
id T68050  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 63..209  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..147  
id AA157130  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 66..195  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98

region 1..130  
id AA094982  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 190..264  
(C) IDENTIFICATION METHOD: blasth  
(D) OTHER INFORMATION: identity 97  
region 5..79  
id W00395  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 59..145  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.9  
seq ALLIVCDVPSASA/QR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ACCCACCCCTC AGACCTAGCC GGAGCAAAGT TTCATTATA GAAGGGAGAG AAGCGAAC | 58  |
| ATG GCA GCG CGT TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG | 106 |
| Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val |     |
| -25 -20 -15                                                     |     |
| GCG CTG CTC ATC GTT TGC GAC GTT CCC TCA GCC TCT GCC CAA AGA AAG | 154 |
| Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys |     |
| -10 -5 1                                                        |     |
| AAG GAG ATG GTG TTA TCT GAA AAG GTT AGT CAG CTG ATG GAA TGG ACT | 202 |
| Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr |     |
| 5 10 15                                                         |     |
| AAC AAA AGA CCT GTA ATA AGA ATG AAT GGA GAC AAG TTC CGT CGC CTT | 250 |
| Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu |     |
| 20 25 30 35                                                     |     |
| GTG AAA GNN CCA CCG AGG                                         | 268 |
| Val Lys Xaa Pro Pro Arg                                         |     |
| 40                                                              |     |

## (2) INFORMATION FOR SEQ ID NO: 245:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 328 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(D) DEVELOPMENTAL STAGE: Fetal  
(F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 45..241  
id H81225  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id H81225  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 2..208  
id W01412  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..199  
id AA044118  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 13..209  
id W42797  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 95..213  
id R39635  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 15..94



id R39635  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 191..286  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq VPMLLLIVGGSFG/LR..

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```

AACAAAGTATG TTACGATGGC TCGATTGCTT TTGCCTAGCG GAAACCATTG ACTAAGGACC 60
GAGCACCAAA TAACCAAGGA AAAGGAAGTG AGTTAAGGAC GTACTCGTCT TGGTGAGAGC 120
GTGAGCTGCT GAGATTTGGG AGTCTGCGCT AGGCCCGCTT CGAGTTCTGA GCCGATGGAA 180
GASTTCACTC ATG TTT GCA CCC GCG GTG ATG CGT GCT TTT CGC AAG AAC 229
 Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn
 -30 -25 -20

AAG ACT CTC GGC TAT GGA GTC CCC ATG TTG TTG CTG ATT GTT GGA GGT 277
Lys Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly
 -15 -10 -5

TCT TTT GGT CTT CGT GAG TTT TCT CNA ATC CGA TAT GAT GCT GTG AAG 325
Ser Phe Gly Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys
 1 5 10

GGG 328
Gly

```

## (2) INFORMATION FOR SEQ ID NO: 246:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..210  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 104..208  
id: AA131932  
est

## (ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 298..342  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 293..337  
id AA131932  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 86..291  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 67..272  
id AA001989  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 29..102  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 11..84  
id AA001989  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 102..331  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 76..305  
id W32996  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 55..96  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 31..72  
id W32996  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 236..377  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 165..306  
id AA121218  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 106..235  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 34..163  
id AA121218  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 70..180
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq LLVLLLYAPVGFC/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

AAGAGCSSCT GCGGCCGGGC GCGAAATGG CGGCGGCGGC GAGGGCCNCG CGCTCCTGAA 60
GCAGCAGTT ATG GAG CTT CCC TCA GGG CCG GGG CCG GAG CGG CTC TTT GAC 111
 Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp
 -35 -30 -25

TCG CAC CGG CTT CCG GGT GAC TGC TTC CTA CTG CTC GTG CTG CTG CTC 159
Ser His Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu
 -20 -15 -10

TAC GCG CCA GTC GGG TTC TGC CTC CTC GTC CTG GGC CTC TTT CTC GGG 207
Tyr Ala Pro Val Gly Phe Cys Leu Leu Val Leu Xaa Leu Phe Leu Gly
 -5 1 5

ATC CAC GTC TTC CTG GTC AGC TGC GCG CTG CCA GAC AGC GTC CTT CGC 255
Ile His Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg
 10 15 20 25

AGA TTC GTA GTG CGG ACC ATG TGT GCG GTG CTA GGG CTC GTG GCC CGG 303
Arg Phe Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg
 30 35 40

CAG GAG GAC TCC GGA CTC CGG GAT CAC AGT GTC AGG GTC CTC ATT TCC 351
Gln Glu Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser
 45 50 55

AAC CAT GTG ACA CCT TTC GAC CAC CAG 378
Asn His Val Thr Pro Phe Asp His Gln
 60 65

```

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..181
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97  
region 1..144  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 186..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 150..276  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 270..311  
id W60505  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 38..312  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..275  
id W60589  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 305..346  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 269..310  
id W60589  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 32..175  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 1..144  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 176..261  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 144..229  
id R33763  
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 268..312  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 238..282  
                           id R33763  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 305..337  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 274..308  
                           id R33763  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 33..176  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 3..146  
                           id AA123856  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 181..346  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
                           region 88..253  
                           id HSB31E112  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 93..181  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
                           region 1..89  
                           id HSB31E112  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 106..375  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.4  
                           seq SLVLLTVTPSXRRQ/QE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

AGGACTTCCC CCGGGCTGAG CTGCGCASGG GGTTTTGGCC AAATTGGGCG AGGGCACAAA 60

ATACCACTT ACCCCTTCTC ACCGAGGAAG AGCGGGAGAA AGGGT ATG GCA CAG TCA 117  
                           Met Ala Gln Ser  
                           -90

DAA GGG TGG GTG RAA AGR TAC KTC AAG GCC TTT TTT AAA GGC TTC TTT 165  
                           Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe C s Lys Gly Phe Phe

|                                                                 |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|
| -85                                                             | -80 | -75 |     |
| GTG GCG GTG CCT GTG GCA GTG ACT TTC TTG GAT CGG GTC GCC TGT GTG |     |     | 213 |
| Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg Val Ala Cys Val |     |     |     |
| -70                                                             | -65 | -60 | -55 |
| GCA AGA GTA GAA GGA GCA TCG ATG CAG CCT TCT TTG AAT CCT GGG GGG |     |     | 261 |
| Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu Asn Pro Gly Gly |     |     |     |
| -50                                                             | -45 |     | -40 |
| AGC NAG TCA TCT GAT GTG GTG SDD DTG AAC CAC TGG AAA GTG AGG AAT |     |     | 309 |
| Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp Lys Val Arg Asn |     |     |     |
| -35                                                             | -30 |     | -25 |
| TTT GAA GTA CAC CGT GGT GAC ATT GTA TCA TTG GTG TTG CTC ACT GTG |     |     | 357 |
| Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val Leu Leu Thr Val |     |     |     |
| -20                                                             | -15 |     | -10 |
| ACG CCC TCC ASC CGA CAA CAG GAG                                 |     |     | 381 |
| Thr Pro Ser Xaa Arg Gln Gln Glu                                 |     |     |     |
| -5                                                              | 1   |     |     |

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 11..158  
id H56585  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 201..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 201..322  
id H56585  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 151..322
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93  
region 119..290  
id AA147898  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 39..159  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 8..128  
id AA147898  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 201..322  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 83..204  
id R52248  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 170..202  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 51..83  
id R52248  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 177..264  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 87..174  
id H54950  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 284..315  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 192..223  
id H54950  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: complement(199..320)  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 40..161  
id W22146  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 67..135  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8.1  
 seq WLLVLSFVFGCNV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```

AGCCGCTGTT GTTGTGGTCC CCATGGAGCT GCCGTAGCGG ACCCAGCACA GCCAGGAGCG 60
TCCGGG ATG AGC TCA GCC GCG GCC GAC CAC TGG GCG TGG TTG CTG GTG 108
 Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val
 -20 -15 -10
CTC AGC TTC GTG TTT GGA TGC AAT GTT CTT AGG ATC CTC CKC CCG GBC 156
Leu Ser Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa
 -5 1 5
YTC STM ATC STG CAK GTC CAG GGT GCT GCA GAA GGA CGC GGA SAG GAG 204
Xaa Xaa Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu
 10 15 20
TCA CAG ATG AGA GCG GAG ATC CAG GAC ATG AAG CAG GAG CTC TCC ACA 252
Ser Gln Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr
 25 30 35
GTC AAC ATG ATG GAC GAG TTT GCC AGA TAT GCC AGG CTG GAN AGA AAG 300
Val Asn Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys
 40 45 50 55
ATC AAC AAG ATG ACG GAT AAG 321
Ile Asn Lys Met Thr Asp Lys
 60

```

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 382 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 196..382  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 98  
 region 10..196  
 id HSC2EA121  
 est

(ix) FEATURE:



(A) NAME/KEY: other  
 (B) LOCATION: 121..205  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 100  
                           region 134..218  
                           id AA095017  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 197..252  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 209..264  
                           id AA095017  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 281..340  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 8  
                           seq HVFFLLLLLAHIIA/LE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

```

GTTTTTGT TT GTGTGTGCGT GTTGTGGGCC TCCATCCCCA CTCCCCAGAC TCCACTTCTC 60
CAGGCCTCTC TCCCGCCTTT TCATCCCGCA TCCGCAGGAC ACCCAATCAC CGGGGCAACA 120
GGATGCCTTC CGCGCCTTCC ACCCTGACCT GGAATTCGTG GCAAGTTCT TGAAACCCCT 180
GCTGATTGGT GAACTGGCCC CGGAGGAGCC CAGCCAGGAC CACGGCAAGA ACTCAAAGAT 240
CACTGAGGAC TTCCGGGCCC TGAGGAAGAC GGCTGAGGAC ATG AAC CTG TTC AAG 295
 Met Asn Leu Phe Lys
 -20

ACC AAC CAC GTG TTC TTC CTC CTC CTC CTG GCC CAC ATC ATC GCC CTG 343
Thr Asn His Val Phe Phe Leu Leu Leu Ala His Ile Ile Ala Leu
-15 -10 -5 1

GAG AGC ATT GCA TGG TTC ACT GTC TTT TAC TTT GCC AAT 382
Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe Gly Asn
 5 10

```

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 80..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 101..321  
id H21228  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 117..357  
id R72127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 77..117  
id R72127  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 60..204  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 63..207  
id H18908  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 195..269  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 199..273  
id H18908  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 23..63  
id H18908  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 65..203  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95

region 144..282  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 19..59  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 98..138  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 252..288  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 333..369  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 228..259  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 90  
region 303..339  
id W93461  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 136..300  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 93..257  
id HUM085F04B  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 170..241  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

|                                                                   |             |
|-------------------------------------------------------------------|-------------|
| AATCACGTGG CTGCCACCCA GGGGCATTCT TCGGGGGTGC ATCAGAGGGA GGCGAGAGCC | 60          |
| TGAGGATCTA AGCGAAGGCT TCCCCGGGTG TAATTCCTG GGCTGTTGT GAGGAGAGAT   | 120         |
| CGAATTCGCC TCCTGCTCTC AGGCCTCTCT GCTCCTGTCT TTTGTTTGG ATG CCG GCG | 178         |
|                                                                   | Met Pro Ala |
| CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG   | 226         |
| Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu   |             |
| -20 -15 -10                                                       |             |

ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT 274  
Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp  
-5 1 5 10  
TCC GGC TCT GGC TAC GTT CCG GGC 298  
Ser Gly Ser Gly Tyr Val Pro Gly  
15

## (2) INFORMATION FOR SEQ ID NO: 251:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (E) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 1..286  
id HUM085F04B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..245
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 167..265  
id R64509  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 118..180  
id R64509  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 245..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 266..307  
id R64509  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 147..262  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 182..297  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 99..161  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 133..195  
id H85714  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 95..286  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 159..350  
id H21228  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 201..286  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 151..236  
id AA009893  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 143..206  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 97..155  
id AA009893  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 99..160  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 49..110  
id AA009893  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..198  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```

ATG ATA GGG TCG GGA TTG GCT GGC TCT GGA GGC GCA GGT GGT CCT TCT 48
Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
 -65 -60 -55

TCT ACT GTC ACA TGG TGC GCG CTG TTT TCT AAT CAC GTG GCT GCM ACC 96
Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr
 -50 -45 -40 -35

CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG CTG CTG CCT 144
Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
 -30 -25 -20

GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTT CTG ACC ATG GCC 192
Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala
 -15 -10 -5

TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT TCC GGC TCT 240
Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser
 1 5 10

GGC TAC GTT CCG GGC TCG GTC TCT GCA GCC TTT GTT ACT TGC CCC AGG 288
Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg
 15 20 25 30

```

## (2) INFORMATION FOR SEQ ID NO: 252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 53..340  
id AA056366  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 80..367  
id R77008  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 77..268  
id W75983  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 269..365  
id W75983  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 129..320  
id W39055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 223..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 321..417  
id W39055  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..236
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 84..288  
id N48534  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 264..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 318..373  
id N48534  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 11..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```

ATTGTTTGG ATG CCG GCG CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG 49
 Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu
 -20 -15

CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AAG CCT CCG ACC CAG 97
Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln
 -10 -5 1 5

CCC TCG CCG GCC TCG GAT TCC GGC TCT GGC TAC GTT CCG GGC TCG GTC 145
Pro Ser Pro Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val
 10 15 20

TCT GCA GCC TTT GTT ACT TGC CCC AAC GAG AAG GTC GCC AAG GAG ATC 193
Ser Ala Ala Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile
 25 30 35

GCC AGG GCC GTG GTG GAG AAG CGC CTA GCA GCC TGC GTC AAC CTC ATC 241
Ala Arg Ala Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile
 40 45 50

CCT CAG ATT ACA TCC ATC TAT GAG TGG AAA GGG AAG ATC GAG GAA GAC 289
Pro Gln Ile Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp
 55 60 65

AGT GAG GTG CTG ATG ATG ATT AAA ACC CAA GCG 322
Ser Glu Val Leu Met Met Ile Lys Thr Gln Ala
 70 75 80

```

## (2) INFORMATION FOR SEQ ID NO: 253:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 247..302  
id T80036  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 33..308



(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.6

seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```

AAGATGGAAC TGGTAGTCAG CTGGAGAGCA GC ATG GAG GCG TCC TGG GGG AGC 53
 Met Glu Ala Ser Trp Gly Ser
 -90

TTC AAC GCT GAG CGG GGC TGG TAT GTC TCT GTG CAG CAG CCT GAA GAA 101
Phe Asn Ala Glu Arg Gly Trp Tyr Val Ser Val Gln Gln Pro Glu Glu
-85 -80 -75 -70

GCG GAG GCC GAA GAG TTG AGT CCG TTG CTA AGC AAC GAA CTT CAC AGA 149
Ala Glu Ala Glu Glu Leu Ser Pro Leu Leu Ser Asn Glu Leu His Arg
 -65 -60 -55

CAG CGA TCC CCA GGT GTT TCA TTT GGT TTA TCA GTG TTT AAT TTG ATG 197
Gln Arg Ser Pro Gly Val Ser Phe Gly Leu Ser Val Phe Asn Leu Met
 -50 -45 -40

AAT GCC ATC ATG GGA AGT GGC ATC CTT GGC TTA GCT TAT GTT ATG GCT 245
Asn Ala Ile Met Gly Ser Gly Ile Leu Gly Leu Ala Tyr Val Met Ala
 -35 -30 -25

AAT ACC GGT GTC TTT GGA TTT AGC TTC TTG CTG CTG ACA GTT GCT CTC 293
Asn Thr Gly Val Phe Gly Phe Ser Phe Leu Leu Leu Thr Val Ala Leu
-20 -15 -10

CTG GCT TCT TAC TCA GTC CAT CTT CTG CTT AGT ATG TGT ATT CAG ACA 341
Leu Ala Ser Tyr Ser Val His Leu Leu Leu Ser Met Cys Ile Gln Thr
-5 1 5 10

GCT GTA ACA TCT TAT GAA GAT CTT GGA CTC TTT GCA TTT GGA TTA CCT 389
Ala Val Thr Ser Tyr Glu Asp Leu Gly Leu Phe Ala Phe Gly Leu Pro
 15 20 25

GGA CTG
Gly Leu
395

```

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..132

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 1..115  
id T10447  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 78..128  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FFLLLRFFLRIDG/VP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

```
ATTTTGAAGA AGTTCTCCTT TTTGAGGATG AACTTCATGA TCATGGAGTT TCAAGCCTGA 60
GTGTGAAGAT TAGAGTA ATG CCT TCT AGC TTT TTC CTG CTG TTG CGG TTT 110
 Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe
 -15 -10

TTC TTG AGA ATT GAG GGG GTG CCG 134
Phe Leu Arg Ile Asp Gly Val Pro
-5 1
```

## (2) INFORMATION FOR SEQ ID NO: 255:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 44..276  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..233  
id N83601  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 51..276  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 15..240  
id N56180  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 69..216  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 23..170  
id R57553  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 46..75  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..30  
id R57553  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 58..142  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 42..126  
id R57171  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 18..56  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 1..39  
id R57171  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 142..182  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 97..137  
id N88966  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 49..83  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..55  
id N88966  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 200..256  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.6  
seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

```

AGTCTTTGTC CTGAGCCAC GATTCCAGAG CTGGCTGGAC CCAAGGAGGT GAAGAGTCAC 60
TTTTCAGCCC CAGGAAGGGC AAAGAAGAGA GARAATCAGC CPGTCTGCTC TCTCCTTGGC 120
TCAACAAGGC CTCTAACAGT CTTCTGTCCT CTATTCTGCA CACGGCATAT TTGGGAACGA 180
GAAACAAAAG TTTTCCCAA ATG AAG AGA ACT CAC TTG TTT ATT GTG GGG ATT 232
 Met Lys Arg Thr His Leu Phe Ile Val Gly Ile
 -15 -10

TAT TTT CTG TCC TCT TGC AGG GCA GAA GAG GGG CTT AAT TTC CCC ACA 280
Tyr Phe Leu Ser Ser Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr
 -5 1 5

TAT GAT GGG AAG GAC CGA GTG GTA AGT CTT TCC GAG AAG AAC TTC AAG 328
Tyr Asp Gly Lys Asp Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys
 10 15 20

CAG GTT TTA 337
Gln Val Leu
25

```

## (2) INFORMATION FOR SEQ ID NO: 256:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 57..182  
id AA019348  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 215..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93  
region 173..287  
id AA019343  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..98

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id AA019348  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 98..217  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 99  
region 57..176  
id AA013099  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 211..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 171..289  
id AA013099  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 43..98  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..56  
id AA013099  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 130..234  
id R54717  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 142..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 58..139  
id R54717  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 95..149  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 10..64  
id R54717  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 105..173  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 1..69  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..267  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 92  
region 108..160  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 296..329  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 185..218  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 167..196  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 93  
region 62..91  
id AA112675  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 88..223  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 91  
region 3..138  
id H27167  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 215..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 129..233  
id H27167  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 145..213  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq VLLLLAALPPVLLP/GA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```

AGAGTGTTTCG CCGCCGCCGC GGCCGCCACC TGGAGTTTCT TCAGACTCCA GATTTCCCTG 60
TCAACCACGA GGAGTCAGA GAGGAAACGC GGAGGAGACA ACAGTACCTG ACGCCTCTTT 120
CAGCCCGGGA TCGCCCCAGC AGGG ATG GGC GAC AAG ATC TGG CTG CCC TTC 171
 Met Gly Asp Lys Ile Trp Leu Pro Phe
 -20 -15
CCC GTG CTC CTT CTG GCC GCT CTG CCT CCG GTG CTG CTG CCT GGG GCG 219
Pro Val Leu Leu Leu Ala Ala Leu Pro Pro Val Leu Leu Pro Gly Ala
 -10 -5 1
GCC GGC TTC ACA CCT TCC CTC GAT AGC GAC TTC ACC TTT ACC CTT CCC 267
Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr Leu Pro
 5 10 15
GCC GGC CAG AAG GAG TGC TTC TAC CAG CCC ATG CCC CTG RAG GCC TCG 315
Ala Gly Gln Lys Glu Cys Phe Tyr Gln Pro Met Pro Leu Xaa Ala Ser
 20 25 30
CTG GAG ATC GAG 327
Leu Glu Ile Glu
 35

```

## (2) INFORMATION FOR SEQ ID NO: 257:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 1..250  
id HSU52870  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 156..311  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..107  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 109..166  
id T35951  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 182..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92  
region 156..302  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 7..107  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 109..166  
id T35949  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 233..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 53..229  
id W17267  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..476
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity  
region 223..295  
id W17267



est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 182..399  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 54..271  
 id HSC34G011  
 est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 136..192  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 7..63  
 id HSC34G011  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 306..416  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.3  
 seq LLSACLVTWGLG/EP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```

AATTCATTTT TCACTCCTCC CTCCTAGGTC ACACTTTTCA GAAAAAGAAT CTGCATCCTG 60
GAAACCAGAA GAAAAATATG AGACGGGGAA TCATCGTGTG ATGTGTGTGC TGCCTTTGGC 120
TKWGTGTGTG GAAGTYCKKG CTCAGGTGTT AGGTACAGTG TGTITGATCG TGGTGGCTTG 180
AGGGGAACCC GCTGTTTACA GCTGTGACTG CGGCTGCACT CAGAGAAGCT GCCCTTGGCT 240
GCTCGTAGCG CCGGGCCTTC TCTCCTCGTC ATCATCCAGA GCAGCCAGTG TCCGGGAGGC 300
ADVNG ATG CCC CAC TCC AGC CTG CAT CCA TCC ATC CCG TGT CCC AGG GGT 350
Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly
 -35 -30 -25

CAC GGG GCC CAG AAG GCA GCC TTG GTT CTG CTG AGT GCC TGC CTG GTG 398
His Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val
 -20 -15 -10

ACC GTT TGG GGG CTA GGA GAG CCA CCA GAG CAC ACT CTC CGG TAC CTG 446
Thr Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu
 -5 1 5 10

GTG CTC CAM CTA GCC TCC CTG CAG CTG GGA 476
Val Leu Xaa Leu Ala Ser Leu Gln Leu Gly
 15 20

```

## (2) INFORMATION FOR SEQ ID NO: 258:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 32..225  
id AA025879  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..154)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 97..250  
id N33067  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(144..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 31..103  
id N33067  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..251  
id AA132495  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 31..251  
id AA063545  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..221)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 47..240

id N99132

est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 59..145
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq HLLLLLLPAPTLK/GL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```

ACACTCGGGC CCCACTCAAG GATGTAGGGC CTTTCTGGC CCGTGACCCC TCCCTGGC 58
ATG GGA GCG TGG GGA CGG GGC TGG CCT TGG GAG GAG CGG CAG GGG CAT 106
Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His
 -25 -20 -15
CAC CTC CTT CTG CTG CTT CTC CCT GCT CCT ACC CTC AAG GGC CTG GGG 154
His Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly
 -10 -5 1
GCT GCC CAG CTG CCT CTA TGC CCT TCT GGG GGT CTC AGC CCA CTG CTG 202
Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu
 5 10 15
ACA CTT CTG CAA TCC GGG
Thr Leu Leu Gln Ser Gly
 20 25

```

## (2) INFORMATION FOR SEQ ID NO: 259:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..429
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 65..433  
id W27019  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(79..429)

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 99  
                           region 91..441  
                           id W26783  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 284..390  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 92  
                           region 343..449  
                           id W85233  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 57..281  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.2  
                           seq LLFIIGLIGCCAT/IR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

ACTCTCGGTG AGCGCRSCCC GCTCTCCGGG CCGGGTCTTC GCGGGCCACC GGCGCC ATG 59
 Met
 -75

GGC CAG TGC GGC ATC ACC TCC TCC AAG ACC GTG CTC GTC TTT CTC AAC 107
Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu Asn
 -70 -65 -60

CTC ATC TTC TGG GGG GCA GCT GGC ATT TTA TGC TAT GTG GGA GCC TAT 155
Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala Tyr
 -55 -50 -45

GTC TTC ATC ACT TAT GAT GAC TAT GAC CAC TTC TTT GAA GAT GTG TAC 203
Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val Tyr
 -40 -35 -30

ACG CTC ATC CCT GCT GTA GTG ATC ATA GCT GTA AGA GCC CTG CTT TTC 251
Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu Phe
 -25 -20 -15

ATC ATT GGG CTA ATT GGC TGC TGT GCC ACA ATC CCG GAA AGT CGC TGT 299
Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg Cys
 -10 -5 1 5

GGA CTT GCC ACG TTT GTC ATC ATC CTG CTC TTG GTT TTT GTC ACA GAA 347
Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Leu Val Phe Val Thr Glu
 10 15 20

GTT GTT GTA GTG GTT TTG GGA TAT GTT TAC AGA GAA AAG GTG GAA AAT 395
Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu Asn
 25 30 35

GAG GTT GAT CGC AGC ATT CAG AAA GTG TAT AAG 428
Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys
 40 45

```

## (2) INFORMATION FOR SEQ ID NO: 260:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 106..364  
id N39913  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..170
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..108  
id N39913  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 39..166  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 183..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94  
region 165..290  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..38  
id HUM527C01B  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 81..275  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7  
 seq IGHFLCLVILVYC/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

AAGAGGATTT GCGGCCCTCC TCTGTGGATT CTGGCCAGGC CGGGTTCGGC GGTGCTGTG 60
AGAGCGGGCT TCCCAACACC ATG CCG KCC GCC TTC TCT GTC AGC TCT TTC CCC 113
 Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro
 -65 -60 -55

GTC AGC ATC CCA GCC GTG CTC ACG CAG ACG GAC TGG ACT GAG CCC TGG 161
Val Ser Ile Pro Ala Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp
 -50 -45 -40

CTC ATG GGG CTG GCC ACC TTC CAC GCG CTC TGC GAG CTC CTC ACC TGC 209
Leu Met Gly Leu Ala Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys
 -35 -30 -25

TTG TCC TCC CGA AGC TAC AGA CTA CAG ATC GGG CAG TTT CTG TGT CTA 257
Leu Ser Ser Arg Ser Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu
 -20 -15 -10

GTC ATC TTA GTC TAC TGT GCT GAA TAC ATC AAT GAG GCG GCT GCG ATG 305
Val Ile Leu Val Tyr Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met
 -5 1 5 10

AAC TGG AGA TTA TTT TCG MAA TAC CAG TAT TTC GAG TCC AGG GGG ATG 353
Asn Trp Arg Leu Phe Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met
 15 20 25

TTC ATT TCT ATA GTA TTT TCA GCC CCA CTG CTG GTG AAT GCC ATG ATC 401
Phe Ile Ser Ile Val Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile
 30 35 40

ATT GTG GTT ATG TGG GTA TGG AAG 425
Ile Val Val Met Trp Val Trp Lys
 45 50

```

## (2) INFORMATION FOR SEQ ID NO: 261:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (11) MOLECULE TYPE: CDNA

## (12) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..165
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90  
region 11..43  
id HUM153A053  
est

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 136..177
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7  
seq LLLSLFFPLRISL/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
ATTTTCTCC GGTACAGCCT GGGAACGTAG GTCCCGCGCC TGTGATAAGT AAGGTTGGAT 60
TTTCTCTTCC CTGAGGTGAA GGATGCCCGG RAGSCCTCGG CAGGACCGCG CGGAAACGGG 120
CCTTCTGCCC AAAAG ATG CTG CTT CTC TCC TTA TTC TTT CCC CTC AGA ATC 171
 Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile
 -10 -5
TCG CTG TCT CCT TCC AAC CAC CTG TGG TCG GCA TCC TCC GGG 213
Ser Leu Ser Pro Ser Asn His Leu Trp Ser Ala Ser Ser Gly
 1 5 10
```

## (2) INFORMATION FOR SEQ ID NO: 262:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..304  
id HSC26A021  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..174

(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 1..158  
id W07871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 205..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 97  
region 192..306  
id W07871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 174..203  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 159..188  
id W07871  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 169..305  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 98  
region 144..280  
id T75539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 64..172  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 41..149  
id T75539  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 175..319  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 161..305  
id H94774  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 24..165  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 94  
region 10..151  
id H94774  
est

## (ix) FEATURE:



(A) NAME/KEY: other  
 (B) LOCATION: 228..319  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 93  
                           region 203..294  
                           id W89738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 43..102  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 91  
                           region 22..81  
                           id W89738  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 82..150  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.6  
                           seq LILVLQLLLRIRR/NR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

ACTCGCACCC GGAACAACAA AGCAAGGAAG ACGGAGTCCG AGCCTCGGGG GCTCCTAGCA 60
ACGGGCCGGG GCGGGAGTTC C ATG GAG ACT GGG GAG CGC GCC CGT CTC ATC 111
 Met Glu Thr Gly Glu Arg Ala Arg Leu Ile
 -20 -15
CTC ATC CTT GTC CTC CAG CTT CTC CTT CGC ATC CGA CGC AAC CGG CAG 159
Leu Ile Leu Val Leu Gln Leu Leu Arg Ile Arg Arg Asn Arg Gln
 -10 -5 1
CAG CGC TGC SCC GCG TCC TCA GCC ACC GCT CCC TTT TCC CAC GGA TGT 207
Gln Arg Cys Xaa Ala Ser Ser Ala Thr Ala Pro Ser Ser His Gly Cys
 5 10 15
GAT CTT CGT GGT GGA AAG CTA AAT TTT AAA ACC ACC CCA ATG GAT GCA 255
Asp Leu Arg Gly Gly Lys Leu Asn Phe Lys Thr Thr Pro Met Asp Ala
 20 25 30 35
GAC AGT GAT GTT GCA TTG GAC ATT CTA ATT ACA AAT GTA GTC TGT GTT 303
Asp Ser Asp Val Ala Leu Asp Ile Leu Ile Thr Asn Val Val Cys Val
 40 45 50
TTT AGA ACA AGA TGT CGG
Phe Arg Thr Arg Cys Arg
 55

```

## (2) INFORMATION FOR SEQ ID NO: 263:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 2..88

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96  
region 18..104  
id R56970  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 128..250

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.4  
seq ILGCSSVCQLCTG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AGGAGTTAAG AAATGTCGTT CTTGAGATTT AAAAAGPAAA CTTTACTGA ATCAGCTGAG 60
TGTTAATAAT ACGAATTTC TTKTCNTGCC AATKCDRMYC TGRDDCAGRA RATCSNWGAA 120
CAGGGWT ATG TGT GGA TTW YAG TTT TCT CTG CCT TGC CTA CGA CTG TTT 169
 Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe
 -40 -35 -30
CTG GTT GTT ACC TGT TAT CKT TTA TTA TTA CTC CAC AAA GAA ATA CTT 217
Leu Val Val Thr Cys Tyr Xaa Leu Leu Leu Leu His Lys Glu Ile Leu
 -25 -20 -15
GGA TGT TCG TCT GTT TGT CAG CTC TGC ACT GGG AGA CAA ATT AAC TGC 265
Gly Cys Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys
 -10 -5 1 5
CGT AAC TTA GGC CTT TCG AGT ATT CTA AGA ATT TTC CTG AAA GTA CAG 313
Arg Asn Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln
 10 15 20
TTT TTC TGT ATC
Phe Phe Cys Ile
 25

```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 176..352  
id W42809  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 50..165  
id W42809  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 116..218  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 34..105  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..285
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 218..260  
id N99674  
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 2..32  
id N99674  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 78..210  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 267..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96  
region 206..303  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..129
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 1..67  
id R20073  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..105.  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..242
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97  
region 105..207  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100  
region 251..281  
id N99685  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..134

id AA154228  
est

## (ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 140..206  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 95  
region 134..200  
id AA154228  
est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 10..228  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.4  
seq ACCFLSAFSPPTLT/KS

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ATAATAAAA ATG AAC CCC GTT ACA GAG TCA CCA TCA TGT CTC TTC TCA CCA | 51  |
| Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro           |     |
| -70 -65 -60                                                       |     |
| CCC TCT GAA TCT GCA TTA GCC AGT CAA CTA GCC CTT TCA GCG TCA TGT   | 99  |
| Pro Ser Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys   |     |
| -55 -50 -45                                                       |     |
| GAC CAG CGC GCC CCA TTC AGC TTG GCT GGT GTC GKT TCA MMA KRA CCC   | 147 |
| Asp Gln Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro   |     |
| -40 -35 -30                                                       |     |
| AGG CTG GCC AGT CGT CAG GTT GCA CCG CCC TTT GGT TCC CGA GCA TGC   | 195 |
| Arg Leu Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys   |     |
| -25 -20 -15                                                       |     |
| TGT TTT CTC TCA GCC TTC TCT CCA ACC TTA ACC AAA TCG GCA GCA GCC   | 243 |
| Cys Phe Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala   |     |
| -10 -5 1 5                                                        |     |
| ACC TCG ACC GCC CAC ACA TTC CTG GCC AAT CAG CTC AGC TGT TTA TTT   | 291 |
| Thr Ser Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe   |     |
| 10 15 20                                                          |     |
| ACC AAA TGT CTT CAC AAC AAC TAC AGC AGC AGC CTT CGG CTA ACA AAA   | 339 |
| Thr Lys Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys   |     |
| 25 30 35                                                          |     |
| AAG CAG GAA AAA TCC ACA ACA CCC CAG                               | 366 |
| Lys Gln Glu Lys Ser Thr Thr Pro Gln                               |     |
| 40 45                                                             |     |

## (2) INFORMATION FOR SEQ ID NO: 265:

## (1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs  
(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 2..86  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 96  
region 8..92  
id AA070287  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 15..80  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 1..86  
id T10748  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 22..88  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 17..83  
id N67981  
est

(ix) FEATURE:

(A) NAME/KEY: other  
(B) LOCATION: 21..85  
(C) IDENTIFICATION METHOD: blastn  
(D) OTHER INFORMATION: identity 100  
region 17..81  
id AA069563  
est

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 25..87  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.3  
seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

AAGGCCGCGG CCGCCAGCGT GGGG ATG TCT AGG AGC TCG AAG GTG GTG CTG 51  
Met Ser Arg Ser Ser Lys Val Val Leu  
-20 -15

GGC CTC TCG GTC CTG CTG ACG GCG GCC ACA GTG GCG GGC GTA CAT GTG 99  
Gly Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val

-10

-5

1

AAG CAG CAG TGG GAC  
Lys Gln Gln Trp Asp  
5

114

## (2) INFORMATION FOR SEQ ID NO: 266:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Muscle

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99  
region 8..204  
id H10448  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..193  
id AA12713  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98  
region 1..193  
id HUML13653  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95  
region 9..205  
id HSC18HC71  
est

## (ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..197

(C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
 region 13..176  
 id AA194682  
 est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 31..108  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.3  
 seq GVGLVTLGLAVG/SY

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

GTCAGGTGGT GGAGGAAAAG GCGCTCCGTC ATG GGG ATC CAG ACG AGC CCC GTC 54
 Met Gly Ile Gln Thr Ser Pro Val
 -25 -20

CTG CTG GCC TCC CTG GGG GTG GGG CTG GTC ACT CTG CTC GGC CTG GCT 102
Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala
 -15 -10 -5

GTG GGC TCC TAC TTG GTT CGG AGG TCC CGC CGG CCT CAG GTC ACT CTC 150
Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu
 1 5 10

CTG GAC CCC AGT GAA AAG TAC CTG CTA CGA CTG CTA GAC AAG ACG ACC 198
Leu Asp Pro Ser Glu Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Thr
 15 20 25 30

CCC GGG
Pro Gly
204

```

## (2) INFORMATION FOR SEQ ID NO: 267:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: CDNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (E) TISSUE TYPE: Muscle

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 33..227  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 95  
 region 1..195  
 id W00881  
 est

## (ix) FEATURE:



(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 167..319  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
 seq VLLSSXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

CATTGCTCT TCTCTTAACT CCTACCTGAA AACCCCATTC CTAATTATT CACTATATTT 60
CAGACTTCTT CACTCTTCTC CMAAACCTG AATCAGCTTG TGCTGATTTT TTCCTATCTG 120
CTATCCCTAA AAGGACTAGA CCTTCTTTCT ATCCTTACTC CCCTCA ATG TAT CCA 175
 Met Tyr Pro
 -50
TCT TAC CTC TTG ATT KKS CCT CCC ATT CCC TCA CAG TTC CTG AAA CAG 223
Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe Leu Lys Gln
 -45 -40 -35
TGC SCC CCC CCG ACC CTA AGC GAC CCC TTT CTG CCC CTG GCC TTG AGG 271
Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu Ala Leu Arg
 -30 -25 -20
TCC CTT GAC GTG CTG CTC CTG TCT TCT GCT CNB YTA GTB VVC NAT TCC 319
Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val Xaa Xaa Ser
 -15 -10 -5
TCT CCC TTG GAA TTC ATC AGA
Ser Pro Leu Glu Phe Ile Arg 340
 1 5

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 368 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 253..332  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 159..238  
 id AA114672  
 est

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide

(B) LOCATION: 195..293  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.2  
 seq ILLXTFQWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AGGGGTACCT GGTGTCATG GCAGGCGGTA TTGACCGAAG AGCTTGRTGA GGAAGAGCAG 60
CTGCTGAGAA GGCATCGCAA AKAGAAGAAG GAGTTGCAAS CCAAAATTCA GGGCATGAAG 120
AATGCTGTTC CCAAGAATGA CAATGAAGAG GDAGGARGCA GCTCACCGRG GATGTGGCCA 180
AGTTGGAAAA AGAW ATG GAA CAG AAA CAY AGA GAS GAA CTG GAG CAA TTG 230
 Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu
 -30 -25

AAG CTG RCT ACT AAG GAG AAT AAG ATT CTG TTG CTG YWA ACA TTT CAA 278
Lys Leu Xaa Thr Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln
-20 -15 -10

ACT TGG TGC TTG AGA ATC AGC CAC CTC GCA TAT CAR AAG CAC AWA AGA 326
Thr Trp Cys Leu Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg
-5 1 5 10

GRC GGG TGC CTG GAT MSA AGG AGC TCT CTG TGT TGT CCT TGG 368
Xaa Gly Cys Leu Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
 15 20 25

```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(1..43)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90  
 region 209..251  
 id AAC13573  
 est

(ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: complement(1..43)  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 90

region 153..195

id AA014924

est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: 54..122

(C) IDENTIFICATION METHOD: Von Heijne matrix.

(D) OTHER INFORMATION: score 5.9  
seq TLKFLTLQKSNA/KR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

AGACGAAGCT CGATGAAGAT TTAGAGAGTT CCAGTGAATC CGATGTGAGT CTG ATG 56
 Met
ATG ACA GCA CCT GTT CTA GCA GCT CAG ACT CTG AAG TTT TTG ACG TTA 104
Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr Leu
 -20 -15 -10
TTG CAG AAA TCA AAC GCA AAA AGG SCC AAC CTT GAG CGA CTT CAT GAT 152
Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His Asp
 -5 1 5 10
GAA CTT TGG TAC AAC GAT CCA GGC CAG ATG AAT GAT GGA CCA CTC TGC 200
Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu Cys
 15 20 25
AAA TGC AGC GCA AAG GCA AGA CGC ACA GGA ATT AGG CAC AGC ATT TAT 248
Lys Cys Ser Ala Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile Tyr
 30 35 40
CCT GGA GAA GAG GCC ATC AAG CCC TGT CGT CCT ATG ACC AAC AAT GCT 296
Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn Ala
 45 50 55
GGC AGA CTT TTC CAC TAC CGG ATC ACA GTM TCC CCG CCT ACG AAC TTT 344
Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn Phe
 60 65 70
TTA ACT GAC AGG CCA ACT GTT ATA GAA TAC GAT GAT CAC GAG TAT ATC 392
Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr Ile
 75 80 85 90
TTT GAA
Phe Glu
 398

```

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 105..208  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 81..184  
                           id N51797  
                           est

## (ix) FEATURE:

(A) NAME/KEY: other  
 (B) LOCATION: 30..110  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 97  
                           region 7..87  
                           id N51797  
                           est

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 54..134  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.9  
                           seq ALALAXAPDLAQA/PL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGTGCAGAAG GTTCTGGGAA GTAGGAGACC CCACTGGCTT TGGTCCCCTA AGA ATG  | 56  |
| Met                                                             |     |
| GAC TCT GCT GCC TGT GCT GCT GCT GCC ACC CCT GTT CCA GCC CTG GCT | 104 |
| Asp Ser Ala Ala Cys Ala Ala Ala Ala Thr Pro Val Pro Ala Leu Ala |     |
| -25 -20 -15                                                     |     |
| TTG GCC HTA GCT CCA GAC CTA GCA CAA GCC CCA CTG GCA CTC CCT GGC | 152 |
| Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro Gly |     |
| -10 -5 1 5                                                      |     |
| CTG TTA AGC CCA TCT TGC CTT CTC TCC TCT GGA CAA GAA GTA AAT GGG | 200 |
| Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn Gly |     |
| 10 15 20                                                        |     |
| AGT GAA AGA GGA ACT TGT CTC TGG AGG CCC TGG CTG TCT TCC ACA AAT | 248 |
| Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr Asn |     |
| 25 30 35                                                        |     |
| GAC TCC CCA AGG CAG ATG AGG AAG CTG GTG GAT TTG GCT GCT GGT GGG | 296 |
| Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly Gly |     |
| 40 45 50                                                        |     |
| GCA ACG GCT GCT GAG GTC ACC AAG GCT GAA TCC ATR NTC CAT CAC CCT | 344 |
| Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His Pro |     |
| 55 60 65 70                                                     |     |
| GTC AGG CTC TTC TGG                                             |     |
| Val Arg Leu Phe Trp                                             | 359 |

## (2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 405 base pairs  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: DOUBLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens  
 (D) DEVELOPMENTAL STAGE: Fetal  
 (F) TISSUE TYPE: kidney

- (ix) FEATURE:  
 (A) NAME/KEY: other  
 (B) LOCATION: 2..304  
 (C) IDENTIFICATION METHOD: blastn  
 (D) OTHER INFORMATION: identity 96  
                                   region 15..317  
                                   id T86266  
                                   est

- (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 64..135  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 5.7  
                                   seq ILGLLGLLGLTLVA/ML

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```

AAAGAGCTTC AGCCTGAAGA CAAGGGAGCA GTCCCTGAAG ACGCTTCTAC TGAGAGGTCT 60
GCC ATG GCC TCT CTT GGC CTC CAA CTT GTG GGC TAC ATC CTA GGC CTT 108
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
 -20 -15 -10
CTG GGG CTT TTG GGS ACA CTG GTT GCC ATG CTG CTC CCC AGC TGG AAA 156
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys
 -5 1 5
ACA AGT TCT TAT GTC GGT GCC AGC ATT GTG ACA GGA GTT GGC TTC TCC 204
Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser
 10 15 20
AAG GGC CTC TGG ATG GAA TGT GCC ACA YAC AGC ACA GGC ATC ACC CAG 252
Lys Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln
 25 30 35
TGT GAC ATC TAT AGC ACC CTT CTG GGC CTG CCC GGT GAC ATC CAG GCT 300
Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala
 40 45 50 55
GCC CAG GCC ATG ATG GTG ACA TCC AGT GCA ATC TCC TCC CTG GCC TGC 348

```

(2) INFORMATION..FOR SEQ ID NO: 272:

- ```

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 324 base pairs
  (B) TYPE: NUCLEIC ACID
  (C) STRANDEDNESS: DOUBLE
  (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Homo Sapiens
  (D) DEVELOPMENTAL STAGE: Fetal
  (F) TISSUE TYPE: kidney

(ix) FEATURE:
  (A) NAME/KEY: other
  (B) LOCATION: 98..326
  (C) IDENTIFICATION METHOD: blastn
  (D) OTHER INFORMATION: identity 100
                        region 15..243
                        id T86266
                        est

(ik) FEATURE:
  (A) NAME/KEY: sig_peptide
  (B) LOCATION: 160..231
  (C) IDENTIFICATION METHOD: Von Heijne matrix
  (D) OTHER INFORMATION: score 5.7
                        seq ILGLLGLLGLTLVA/ML

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

| | | | | | | |
|---|------------|------------|------------|---------------------|------------|-----|
| AGCTGCTTGT | GGCCACCCAC | AGACACTTGT | AAGGAGGAGA | GAAGTCAGCC | TGGCAGAGAG | 60 |
| ACTCTGAAAT | GASSGATTAG | AGGTGTTCAA | GGRAGCAAAG | AGCTTCAGCC | TGAAGACAAG | 120 |
| GGAGCAGTCC | CTGAAGACGC | TTCTACTGAG | AGGTCTGCC | ATG GCC TCT CTT GGC | ... | 174 |
| | | | | Met Ala Ser Leu Gly | | |
| | | | | -20 | | |
| CTC CAA CTT GTG GGC TAC ATC CTA GGC CTT CTG GGG CTT TTG GGC ACA | | | | | | 222 |
| Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu Gly Leu Leu Gly Thr | | | | | | |
| | -15 | | -10 | | -5 | |
| CTG GTT GCC ATG CTG CTC CCC AGC TGG AAA ACA AGT TCT TAT GTC GGT | | | | | | 270 |
| Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr Ser Ser Tyr Val Gly | | | | | | |

| | | | |
|---|----|----|-----|
| 1 | 5 | 10 | |
| GCC AGC ATT GTG ACA GCA GTT GGC TTC TCC AAG GGC CTC TGG ATG GAA | | | 318 |
| Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys Cys Leu Trp Met Glu | | | |
| 15 | 20 | 25 | |
| TGT GCC | | | |
| Cys Ala | | | 324 |
| 30 | | | |

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 19..184
id AA132585
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..54
id N57441
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 272..325
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

| | |
|--|-----|
| ACGCAGCCGT CAGCCGAACA ATTCGATGAC GAGGCCCAGG AAGCACCCTG AAACCCCTGGG | 80 |
| CGGCGGCAAG CTGTGCGACC TCCTCTGCGG CCGGCCTGGA CTAGCTTTAT CGTCATCTGG | 120 |
| GAAATTGTTA AAAATGCAAA TTCGCAAGTT TGAGAGCCAT GGTCCAAGA AACTGCATAA | 160 |

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 15..250
id H23844
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 8..237
id AA036876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 21..251
id H22656
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..217
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..183
id W05714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 218..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 183..219
id W05714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..211
id AA100765
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 69..152
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

```

ACGTGACCGG GGCCTGAAGC CGGAAGCTAC CTATCTGGTA GGGAGCTCCC CCAGCACCGA    60
AGACTGCG ATG ACT TCT GCA CTG ACC CAG GGG CTG CAG CGA ATC CCA GAC    110
      Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp
                -25                      -20                      -15

CAG CTC GGC TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT    158
Gln Leu Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser
                -10                      -5                      1

GGG GAC CTG GAG AAT GAT GAG CAG GCA DCC AGT GCC ATC TCT GAG CTG    206
Gly Asp Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu
                5                      10                      15

GTC AGC ACA GCC TGC GGT TTC CGG CTG CAC CGC CCG ATG AAT GTG CCC    254
Val Ser Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro
                20                      25                      30

AGG
Arg
35

```

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..243

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 6..245
id H6405C
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..248
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..234
id R17172
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..248
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..235
id HSC15C081
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..248
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..227
id AA149663
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 43..248
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 29..234
id HSU46380
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..149
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq ITGVILLAVGIWG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

```
AGGTGCAGGG TCTCGGGCTA GTC ATG GCG TCC CCG TCT CGG AGA CTG CAG ACT   53
                        Met Ala Ser Pro Ser Arg Arg Leu Gln Thr
                        -40                               -35

AAA CCA GTC ATT ACT TGT TTC AAG AGC GTT CTG CTA ATC KAC ACT NTK   101
Lys Pro Val Ile Thr Cys Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa
-30                               -25                               -20

ATT TKC TGG ATC ACT GGC GTK ATC CTT CTT GCA GTT GGC ATT TGG GGC   149
```

```

Ile Xaa Trp Ile Thr Gly Val Ile Leu Leu Ala Val Gly Ile Trp Gly
-15                      -10                      -5
AAG GTG AGC CTG GAG AAT TAC TTT KCK CTT TTA AAT GAG AAG GCC ACC 197
Lys Val Ser Leu Glu Asn Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr
1                      5                      10                      15
AAT GTC CCC TTC GKG CTC ATT GCT ACT GGT ACC GTC ATK ATT CTT TTG 245
Asn Val Pro Phe Xaa Leu Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu
20                      25                      30
GGC TAC CGG
Gly Tyr Arg
35
254

```

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 37
region 19..246
id HUMHG1206
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..222
id C15962
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 35..220
id HUM417F078
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 2..33
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..32
 id HUM417F07B
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 59..228
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 18..187
 id AA139623
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 94..178
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..85
 id N83476
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 177..228
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 82..133
 id N88476
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 49..108
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.3
 seq VLLGSSTILSQP/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```

GTCGCTTGGT GGCTCCGTCT GTCTGTCCGT CCGCCCGCGG GTGCCATC ATG GCG GAC   57
                                     Met Ala Asp
                                     -20

GCG GCC AGT CAG GTG CTC CTG GGC TCC GGT CTC ACC ATC CTG TCC CAG   105
Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile Leu Ser Gln
   -15                               -10                               -5

CCG CTC ATG TAC GTG AAA GTG CTC ATC CAG GTG GGA TAT GAG CCT CTT   153
Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr Glu Pro Leu
   1                               5                               10                               15

CCT CCA ACA ATA GGA CGA AAT ATT TTT GGG CGG CAA GTG TGN YAG CTT   201
Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val Xaa Xaa Leu
   20                               25                               30

CCT NGT CTC TTT AGT TAT GCT CAG CAC GGG                               231

```

Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly
35 40

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..185)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 93..276
id AA136898
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..89
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 30..76
id W96077
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..161
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 110..146
id W96077
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 83..119
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 69..105
id W96077
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 1..35

id W96077
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 126..161
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 129..164
id N41630
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 58..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 63..94
id N41630
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..31
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 7..36
id N41630
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 38..161
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 19..142
id AA043148
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 121..185
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 61..125
id HUM430A04B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..119
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..60
id HUM430A04B
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 98..157
(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```

AACCTCTTCC GAGCGGGGTC ACGGCCCCGC CGTCGGTAAC CTGGTTTCCG AGAGTGCCGG      60
GCGGTCGGCG GGTCAGGGCA GCCCGGGGCC TGACGCC ATG TCC CGG AAC CTG CGC      115
                               Met Ser Arg Asn Leu Arg
                               -20                               -15

ACC GCG CTC ATT TTC GGC GGC TTC ATC TCC CTG ATC GGC GCC GCC TTC      163
Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser Leu Ile Gly Ala Ala Phe
          -10                               -5                               1

TAT CCC ATC TAC TTC CGA CCC CAT GGG                                  190
Tyr Pro Ile Tyr Phe Arg Pro His Gly
          5                               10

```

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(97..229)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 10..142
id H62783
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 54..192
id T71240
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 352..429

id AA075451
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 80..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 288..348
id AA075451
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..222
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 350..437
id AA009954
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 105..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 319..354
id AA009954
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 148..216
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 384..452
id W15396
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 80..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 315..352
id W15396
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 206..256
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LWCFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

ATGAGTGTG ATGTTTTCT GCACTAGAAG GCACTATGTT GAACTATTAA ACTTACCAGC 60
ACTTCTTTT TCCACTCCAT AGTTTCATTG TACTGACAAC CTCAGCTGGC ATCATGGACC 120

```

ATGAAGAAGC AAGACGAAAA CACACAGGRA GGGAAATCC TGGGATTCTT TTTCTAGGGA 180
TGTAATACAT ATATTACAA ATAAA ATG CCT CAT GGA CTC TGG TGC TTC CAC 232
                Met Pro His Gly Leu Trp Cys Phe His
                -15                               -10
TTG GTC GTT TTG AGC CTT TAC AGC AGT GTA GCC ACA GCC CGG 274
Leu Val Val Leu Ser Leu Tyr Ser Ser Val Ala Thr Ala Arg
                -5                               1                               5

```

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..124)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 104..226
id W94087
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 12..134
id R37206
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 19..141
id N42384
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..92)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 16
region 17..267

id H84930
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(81..124)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 144..187
id H84930
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(2..124)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 148..270
id H82795
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 21..62
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq SLVAVFLSCGLIS/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
ATAAATTAGC AGTATTAGTT ATG AGT TTG GTT GCA GTG TTC TTA TCT TGT GGG    53
                Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly
                               -10                               -5

CTG ATT TCC AAA AAC CAC ATG CTG CTG AAT TTA CCA GGG ATC CTC ATA    101
Leu Ile Ser Lys Asn His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile
      1                               5                               10

CCT CAC AAT GCA AAC CAC TTA CTG
Pro His Asn Ala Asn His Leu Leu
    15                               20

                               125
```

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(E) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 2..85
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 4..37
 id HUML1521
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 85..120
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 86..121
 id HUML1521
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 89..148
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 123..182
 id W52706
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 34..84
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 69..119
 id W52706
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(75..148)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 324..397
 id AA132959
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 27..98
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq GALAVGAVPVVLS/AM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```

AAAGTTGNSA CCCGGACGGC CTCACC ATG ATG AAA CGG GCA GCT GCT GCT GCA    53
               Met Met Lys Arg Ala Ala Ala Ala Ala
                        -20

ATG GGA GGA GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG CTC AGT GCC    101
Val Gly Gly Ala Leu Ala Val Gly Ala Val Pro Val Val Leu Ser Ala
-15                -10                -5                1

```

ATG GGC TTC ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA GCA GCC CAT 149
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala His
 5 10 15

GGG
 Gly 152

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
 region 14..212
 id H14129
 est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 19..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
 seq LISFSWFANYIRA/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

ATTGCCCTCA TTGCCGGC ATG GCC GTC ATT GTG GAT AAA CCC TGG TTC TAT 51
 Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr
 -80 -75

GAC ATG AAG AAA GTT TGG GAG GGA TAT CCC ATA CAG AGC ACT ATC CCT 99
 Asp Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro
 -70 -65 -60 -55

TCC CAG TAT TGG TAC TAC ATG ATT GAA CTT TCC TTC TAC TGG TCC CTG 147
 Ser Gln Tyr Trp Tyr Tyr Met Ile Glu Ser Phe Tyr Trp Ser Leu
 -50 -45 -40

CTC TTC AGC ATT GCC TCT GAT GTC AAG CGA AAG GAT TTC AAG GAA CAG 195
 Leu Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln
 -35 -30 -25

ATC ATC CAC CAT GTG GCC ACC ATC ATT CTC ATC AGC TTT TCC TGG TTT 243
 Ile Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe

| | | | |
|---|-----|-----|-----|
| -20 | -15 | -10 | |
| GCC AAT TAC ATC CGA GCT GGG ACT CTA ATC ATG GCT CTG CAT GAC TCT | | | 291 |
| Ala Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser | | | |
| -5 | 1 | 5 | 10 |
| TCC GAT TAC CTG CTG GAG TCA GCC AAG ATG TTT AAC TAC GCG GGA TGG | | | 339 |
| Ser Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp | | | |
| 15 | 20 | 25 | |
| AAG AAC ACC TGC AAC AAC ATC TTC ACC GTC TTC GCC ATT GTT TTT ATC | | | 387 |
| Lys Asn Thr Cys Asn Asn Ile Phe Thr Val Phe Ala Ile Val Phe Ile | | | |
| 30 | 35 | 40 | |
| ATC ACC CGA CTG GTC ATC CTG CCC TTC TGG ATC CTG CAT TGC | | | 429 |
| Ile Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys | | | |
| 45 | 50 | 55 | |

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 37..147
id T82645
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 35..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLFIYIFLTCSNT/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

| | |
|---|-----|
| ATAGTATCTA TTGAAAAGGA AGCAGTGTGT ATCT ATG ATT ATA TCT CTG TTC ATC | 55 |
| Met Ile Ile Ser Leu Phe Ile | |
| -15 | -10 |
| TAT ATA TTT TTG ACA TGT AGC AAC ACC TCT CCA TCT TAT CAA GGA ACT | 103 |
| Tyr Ile Phe Leu Thr Cys Ser Asn Thr Ser Pro Ser Tyr Gln Gly Thr | |
| -5 | 1 |
| 5 | |

| | |
|---|-----|
| CAA CTC GGT CTG GGT CTC CCC AGT GCC CAG TGG TGG CCT TTG ACA GGT | 151 |
| Gln Leu Gly Leu Gly Leu Pro Ser Ala Gln Trp Trp Pro Leu Thr Gly | |
| 10 15 20 | |
| AGG AGG ATG CAG TGC TGC AGG CTA TTT TGT TTT TTG TTA CAA AAC TGT | 199 |
| Arg Arg Met Gln Cys Cys Arg Leu Phe Cys Phe Leu Leu Gln Asn Cys | |
| 25 30 35 | |
| CTT TTC CCT TTT CCC CTC CAC CTG ATT CAG CAT GAT CCC TGT GAG CTG | 247 |
| Leu Phe Pro Phe Pro Leu His Leu Ile Gln His Asp Pro Cys Glu Leu | |
| 40 45 50 55 | |
| GTT CTC ACA ATC TCT GGG ACT | |
| Val Leu Thr Ile Ser Gly Thr | 268 |
| 60 | |

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..248
id HSC20D111
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 122..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..136
id T77096
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..146
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..147
id N32450
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 9..104
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LQMLLG FVGRSKS/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AGACCAAG ATG GCG GCG GAG CTG GTG GAG GCC AAA AAC ATG GTG ATG AGT    50
      Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser
            -30                    -25                    -20

TTT CGA GTC TCC GAC CTT CAG ATG CTC CTG GGT TTC GTG GGC CGG AGT    98
Phe Arg Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser
            -15                    -10                    -5

AAG AGT GGA CTG AAG CAC GAG CTC GTC ACC AGG GCC CTC CAG CTG GTG   146
Lys Ser Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val
            1                      5                      10

CAG TTT GAC TGT AGC CCT GAG CTG TTC AAG AAG AAG AAG GAG CTG TAC   194
Gln Phe Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr
            15                    20                    25                    30

GAG ACC CGC TAC GCC AAG AAG AAC TCG GAG CCT GCC CCA CAG CCG CAC   242
Glu Thr Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His
            35                    40                    45

CGG CCC CTG GAC CCC CTG ACC GGG
Arg Pro Leu Asp Pro Leu Thr Gly
            50

```

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..105
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..96
id R05622
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 24..92
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 2..70
 id H94933
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 64..243
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq VHALCPLSPLVT/GC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```

AACTCTCCAA AAAGCAGAGA CAGCAGGAAG AGGGGAGTGG AGGCAGCCCA TTCACCTGGG      60
GAA ATG ACT GGG TTG TCG ATG GMC GGT GGC GGB AGC CSA AMG GGG GAY      103
Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp
-60                      -55                      -50

GTG GAS CCG TDC TAC TAT GGT AAR CVT GGG CCC CTG CGC RCC CTT CCT      156
Val Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro
-45                      -40                      -35                      -30

GAG CCC TCA GGA CCC CTT CCA CCA AGC AGC GGC CTC TCC CAG CCC CAG      204
Glu Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln
-25                      -20                      -15

GTC CAT GCT CTG TGC CCC TTA TCT CCC CTG GTT ACC ACG GGC TGC TGC      252
Val His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys
-10                      -5                      1

GGG CAG GCT GCG
Gly Gln Ala Ala
5
264

```

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 157..269
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 95..207
id N41379
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..112
id N41379
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 275..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 213..257
id N41379
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 8..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..166
id AA044371
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 157..219
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 149..211
id AA044371
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(272..319)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 423..470
id N30852
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(225..264)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 478..517
id N30852
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(320..349)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 394..423
 id N30852
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(238..271)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 481..514
 id AA044232
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 303..349
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 5..51
 id R78468
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 367..459
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq GLLGXGLXXXSLT/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AAAGTCCTAG AGGGGGTCGG GGTMTGGGTG GACAAGCTTT CCTCGTCCTC TCCCNACAGA   60
GCTGACGTGT CCTGGGTTCC ACCGGGAGCG GGCATTTCOA CCGGACGGGA GGGTTCGGGG   120
TGTCCGGGGC TGGGAATAC GTARGGKGTG CSGCGCCGGT GTGGGAAGTT GGGGCGTGTG   180
GCTGCAGTCC CGGGAGTTCT TGGAGGGGGT CGGCCACCG AGCTTCCGGA CCGGCTGATC   240
TCCCCGTAGC TTGCCGGAGG GAGGGCGGAG CTGACTCTCC GTCCCTTCTC CCATCCCCCTC   300
SAGTGGTGGG TACGGGCACC TCGCTGGCGC TCTCCTCCCT CCTGTCCCTN GNNSNTCTTT   360
GCTGGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC AMC GAG TGG CTC   403
      Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu
      -30                      -25                      -20

ACC ATC CAG GGC GGC CTG CTT GGW KCG GGT CTC TTS KRG TYC TCG CTC   456
Thr Ile Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu
      -15                      -10                      -5

ACT GCG GGG
Thr Ala Gly
1

```

465

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 56..337
id AA203498
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..65
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..59
id AA203498
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 344..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 338..379
id AA203498
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 44..273
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..344
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 274..326
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 20..65
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..47
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 344..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 327..368
id W87295
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..312
id AA248429
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 344..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 313..354
id AA248429
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 76..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..269
id W01758
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 344..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 270..311
id W01758
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 30..201
id AA249637
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 33..65
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..33
 id AA249637
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 257..289
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 222..254
 id AA249697
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 227..256
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 193..222
 id AA249697
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 19..180
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq LIVWLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

| | |
|---|-----|
| ATCTGGCTCA GTTCCGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC | 51 |
| Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg | |
| -50 -45 | |
| AGG TCT CGG CGG GAG CTG GAA GTG CGC AGT CCA CAA CAG AAC AAA TAT | 99 |
| Arg Ser Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr | |
| -40 -35 -30 | |
| TCG GTG CTT TTA CCT ACC TAC AAC GAG CGC GAG AAC CTG CCG CTC ATC | 147 |
| Ser Val Leu Leu Pro Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile | |
| -25 -20 -15 | |
| GTG TGG CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA | 195 |
| Val Trp Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu | |
| -10 -5 1 5 | |
| ATT ATA ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT | 243 |
| Ile Ile Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala | |
| 10 15 20 | |
| GAA CAG TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA | 291 |
| Glu Gln Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro | |
| 25 30 35 | |

CGA GAG AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CDY SRA ATG AAA 339
Arg Glu Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys
40 45 50

CAT GCA CAG GAA ACT ACA TCA TTA TTA TGG ATS CTG ATC TCT CAC 384
His Ala Gln Glu Thr Thr Ser Leu Leu Trp Xaa Leu Ile Ser His
55 60 65

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..268
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 13..245
id AA134651
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 244..281
id AA134651
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..272
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 95..353
id W26888
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 7..208
id T66207
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 263..325.
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 208..270
 id T66207
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 39..267
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 1..229
 id W00383
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 35..304
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 13..282
 id HSC36A071
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 207..266
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.3
 seq LLDSSLMASGTAS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

```

AAACCGGGK TAGACGTACC TCACGGAGC CGGCTTTGGC CCGCGGCTK YTACCGTCCG      60
CGCGGAGAAA TTGTTGGATC TGGCAGTCTA GGAATGAATC TCTCTCAGC CTTTAAGCTC    120
ACCTGGTCAG AATCCTTGA TGAGCCTGTG GGACCGTTCC TCTAGCCCG GTGSTTTGGA    180
ACCACTGGCT TTGGGACTGT AAGAGG ATG GAC AAA GAT TCT CAG GGG CTG CTA      233
                        Met Asp Lys Asp Ser Gln Gly Leu Leu
                        -20                               -15

GAT TCA TCC CTG ATG GCA TCA GGC ACT GCC AGC CCG TCA GAG GAT GAG      281
Asp Ser Ser Leu Met Ala Ser Gly Thr Ala Ser Arg Ser Glu Asp Glu
-10                               -5                               1                               5

GAG TCA CTG GCA GGG CAG AAG CGA GCC TCC TCC CAG GCC CTG GGC ACC      329
Glu Ser Leu Ala Gly Gln Lys Arg Ala Ser Ser Gln Ala Leu Gly Thr
                        10                               15                               20

GGG
Gly
                                                                 332

```

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 38..138
id AA009514
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 161..252
id AA009514
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..131
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 15..44
id AA009514
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 100..207
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CLAVSWEAAGCHG/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

AAAGGAATAC TGACAGATAA GGCCGGAAAC AAAACTGATG GATTGAAAAA CATTTTATG      60
GAATGTATTT ACTATCATTT TGTTTTACTA TAGAGGTAG ATG GGA CTC TTA ACT      114
                                     Met Gly Leu Leu Thr
                                     -35
TTT GGG TAC APT GAA AMC AKG CKG AAA ACT GAA CAC AAT CCT GAT CAT      162
Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu His Asn Pro Asp His
-30                               -25                               -11

```

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 73..208
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100.00
region 53..188
id T06781
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 20..80
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..61
id T06781
est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 16..105
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..90
 id AA101354
 est

(2x) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 12..59

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.1

seq YAAVAGVLAVES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AGCGCGGGAA C ATG GGG CTG TAC GCT GCG GTG GCA GGC GTG CTG GCC GGC      50
      Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly
      -15                      -10                      -5

GTG GAG AGC CGC CAG GGC TCT AAT CAA GGG GCT GGT GTA CTC CAG CAA      98
Val Glu Ser Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln
      1                      5                      10

CTT CCA GAA CGT GAA RCA GCT GTA CGC GCT GGT GTG CGA AAS GCA GCG      146
Leu Pro Glu Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala
      15                      20                      25

CTA CTC CGC CGT GCT GGA TRC CGT GAT CTC CAR CGG CGG CCT CCT CAG      194
Leu Leu Arg Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln
      30                      35                      40                      45

TGC GAA GAA GCT
Cys Glu Glu Ala
                                         206

```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 26..219

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91
region 1..194
id T06781
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 204..234

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 176..206
id T06781
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 22..74
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 1..53
 id AA101354
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 71..110
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 51..90
 id AA101354
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..203
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq LDAVIASAGLLRA/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

| | |
|---|-----|
| AAAAGGCGCG CGGGAAC ATG GGG CTG TAT GCT GCA GCT GCA GGC GTG TTG | 50 |
| Met Gly Leu Tyr Ala Ala Ala Gly Val Leu | |
| -60 -55 | |
| GCC GGC GTG GAG AGC CGC CAG GGC TCT ATC AAG GGG TTG GTG TAC TCC | 98 |
| Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser | |
| -50 -45 -40 | |
| AGC AAC TTC CAG AAC GTG AAG CAG CTG TAC GCG CTG GTG TGC GAA ACG | 146 |
| Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr | |
| -35 -30 -25 -20 | |
| CAG CGC TAC TCC GCC GTG CTG GAT GCT GTG ATC GCC AGC GCC GGC CTC | 194 |
| Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu | |
| -15 -10 -5 | |
| CTC CGT GCG GAG AAG AAG CTG CGG CCG CAC CTG GCC AAG GTG CTA GTG | 242 |
| Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys Val Leu Val | |
| 1 5 10 | |
| TAT GAG TTG TTG TTG GGA AAG GGC TTT CGA GGG GGT GGG GGC CGA TGG | 290 |
| Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly Gly Arg Trp | |
| 15 20 25 | |
| AAG GCC CGG | 299 |
| Lys Ala Arg | |
| 30 | |

(2) INFORMATION FOR SEQ ID NO: 292:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..458
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..163
id R50658
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(413..458)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 442..487
id AA016001
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 5..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

| | |
|--|-----|
| AGAA ATG GGT GCT CAG CAC ACA GCA CTT CTT CTA AAT ACA GAG GTG AGG | 49 |
| Met Gly Ala Gln His Thr Ala Leu Leu Asn Thr Glu Val Arg | |
| -60 -55 -50 | |
| TGG CTT TCT CGA GGT AAA GTT CTT GTA AGA CTT TTT GAA CTT CGT CGT | 97 |
| Trp Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg | |
| -45 -40 -35 | |
| GAA CTT TTG GTT TTC ATG GAT TCT GCT TTT CGA CTA TCT GAT TGT TTA | 145 |
| Glu Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu | |
| -30 -25 -20 | |
| ACA AAT TCA TCT TCG CTG CTA AGA CTT GCA TAT CTT GCA GAT ATT TTT | 193 |
| Thr Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe | |
| -15 -10 -5 | |
| ACT AAA TTA AAT GAA GTT AAT TTG TCA ATG CAA GCA AAA AAT GTG ACC | 241 |
| Thr Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr | |
| 1 5 10 15 | |
| GTG TTT ACA GTA TTT GAT AAA ATG TCG TCA TTG TTA AGA AAA TTG GAA | 239 |

```

Val Phe Thr Val Phe Asp Lys Met Ser Ser Leu Leu Arg Lys Leu Glu
      20                      25                      30
TTT TGG GCC TCA TCT GTA GAA GAA GAA AAC TTT GAT TGT TTT CCT ACA    337
Phe Trp Ala Ser Ser Val Glu Glu Glu Asn Phe Asp Cys Phe Pro Thr
      35                      40                      45
CTC AGT GAT TTT TTG ACT GAA ATT AAT TCT ACA GTT GAT AAA GAT ATT    385
Leu Ser Asp Phe Leu Thr Glu Ile Asn Ser Thr Val Asp Lys Asp Ile
      50                      55                      60
TGC AGT GCC ATT GTG CAG CAC CTA AGG GGT TTG CGC GCT ACT CTG TTA    433
Cys Ser Ala Ile Val Gln His Leu Arg Gly Leu Arg Ala Thr Leu Leu
      65                      70                      75
AAA TAC TTT CCT GTA ACA AAT GAC
Lys Tyr Phe Pro Val Thr Asn Asp    457
      80                      85

```

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..206
id AA044042
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 6..183
id AA127902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..160
id AA056679
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(99..247)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 302..450
id W93399
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 11..158
id R29154
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 117..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LVVMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

```

AATCCGCGGC AGAGCGGCTG CTTGAGATCT GTTTCTGGGG CCTCTGGCGG TGGCGGCCTG      60
TGGCGGCCTG GGGCGGCGCG ACGGCTGGTG CGCAGGTACA CTGATGCTGA AGTACT ATG      119
                                         Met
                                         -25

AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT GTT ATG GTC      167
Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met Val
      -20                      -15                      -10

CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC AGC      215
Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser Ser
      -5                      1                      5

CCT GTT TTC CAA ATA CCT AAA AAC GAC AAC ATG      248
Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 245..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 20..149
id T41381
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 75..227
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

```

AAAAATAAAA TGTAGGCAGC AAAAGTGGAA CAGGAGAGGC AGCTGGTGCA CTAATCCAGG      60
TCAGCAATCT GAAG ATG GTC TTA CGG AGC CTA GTA GAG TAC TCC CAG GAT      110
      Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp
      -50                      -45                      -40
GTC CTG GCG CAT CCT GTG TCA GAA GAG CAT CTC CCA GAT GTG AGC CTC      158
Val Leu Ala His Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu
      -35                      -30                      -25
ATT GGA GAG TTC TCA GAC CCG GCA GAG CTC GGC AAG CTG CTT CAG CTG      206
Ile Gly Glu Phe Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu
      -20                      -15                      -10
GTS CTG GGC TGT GCC ATC AGT TGC GAG AAA AAG CAG GAC CAC ATC CAG      254
Val Leu Gly Cys Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln
      -5                      1                      5
AGA ATC ATG ACG CTG GAA GAA TCG GTT CAG CAT GTS GTG ATG GAA GCC      302
Arg Ile Met Thr Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala
      10                      15                      20                      25
ATC CAA GAG CTC ATG ACC AAA GAC ACT CCT GAC TCC CTG TCA CCA GAG      350
Ile Gln Glu Leu Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu
      30                      35                      40
AGG TAT GGC AAC TTT GAC AGC CAG TCC CGC AGT ACT GGG      389
Thr Tyr Gly Asn Phe Asp Ser Gln Ser Arg Ser Thr Gly
      45                      50

```

(x) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 105..270
id AA084830
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 64..93
id AA084830
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 66..231
id W01570
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 26..53
id W01570
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 296..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..111
id H82170
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 298..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 7..115
id N71014
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(147..201)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 236..292
id N35296
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 358..396
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq MIHGFLAPTSTA/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```
ATGGGGGCGG ASTAGCCGGA GCCGCGAGTC CATTTTGGGG CTGTGCTTGG CGCGTACCGT   60
GCGGTCCCTG TAGTTGGAGG ACGGGCGGTC GCGCSGGCCT TTCCCACTAG CCGGAGGTGG   120
GAGATAAGTA CCCGCCGCCC GGCTTCTCTC GGGAAAGCGG GGTGGTCCTC GAACCTTCAG   180
CGAGGGTGGG GAGTTGCCCA GTAGCCTCTA GTTCGTTAGT CAAAACGTGA AAAAAAAGA   240
CCTGCTTTGC CVTGGGAAAT AGTAACCCTG CCAAATACAT CAGCTTGTAG GAGACAGAGG   300
ATGTGATGGA GCTGCTTGAA GAAGATCTCA CATGCCCTAT TTGTTGTAGT CTGTTTG   357
ATG ATC CAC GGG TTT TGC CTT GCT CCC ACA ACT TCT GCA AAA AAT GCT   405
Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala
      -10                      -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..86
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..63
id C16693
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 25..86
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 9..70
 id H48377
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 38..86
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 36..84
 id R17245
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 38..86
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 7..55
 id H19182
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(19..54)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 181..216
 id T12463
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 90..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq RTWCLAGVEASPG/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

```

AAGCCTGGGA CACCGCCGGC GGGGAGAGAA GCGGATCCCG TCGAGCCCC GGCCCCAAGT   60
AAGCCCGCCG CCCCGGAGCC GCCGTGAGT ATG CYT TGT CCC AGG ACC TGG TGT   113
                               Met Xaa Cys Pro Arg Thr Trp Cys
                               -15                               -10
CTC GCC TGC GTT GAA GCA TCT CCA GGG CAG CCC TTC CTC CCG CCC CGC   161
Leu Ala Cys Val Glu Ala Ser Pro Gly Gln Pro Phe Leu Pro Pro Arg
                               -5                               1                               5
CCC GGG
Pro Gly                               167

```

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 93..226
id W81645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 31..95
id W81645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 62..195
id W06951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 7..64
id W06951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..222
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..179
id W38711
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

- (B) LOCATION: 24..86
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

```

GCNGTCGGCT CCGCGGCGCC GCC ATG GCC GAC GTG GAA GAC GGA GAG GAA ACC   53
      Met Ala Asp Val Glu Asp Gly Glu Glu Thr
      -20                               -15

TGC GCC CTG GCC TCT CAC TCC GGG AGC TCA GGC TCC AAG TCG GGA GCC   101
Cys Ala Leu Ala Ser His Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly
  -10                               -5               1               5

GAC AAG ATG TTC TCC CTC AAG AAG TGG AAC GCG GTG GCC ATG TGG AGC   149
Asp Lys Met Phe Ser Leu Lys Lys Trp Asn Ala Val Ala Met Trp Ser
      10                               15               20

TGG GAC GTG GAG TGC GAT ACG TGC GCC ATC TGC AGG GTC CAG GTG ATG   197
Trp Asp Val Glu Cys Asp Thr Cys Ala Ile Cys Arg Val Gln Val Met
      25                               30               35

GAT GCC TGT MTT AGA TGT CAA GCG GGG   224
Asp Ala Cys Xaa Arg Cys Gln Ala Gly
      40                               45
  
```

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: 122..188
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 198..264
 id R58050
 est

(ix) FEATURE:

- (A) NAME/KEY: other
 (B) LOCATION: complement(122..188)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 193..259
 id H98670

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(122..188)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 194..260
 id N66980
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(122..188)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 198..264
 id AA159781
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(122..188)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 161..227
 id H45410
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 273..350
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq IIMFLLIIVCGSP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

TAGAAGTAGC AGGATCGCCT TAATAATAAT AATAGTTTTG TAGCATGAAG CCTGAGCATT   60
GTCCAAAGTT TGGAAATGTG AACGCTGATA GTCACATCTG TCCATCTTTC CACATTCTTA   120
GGATGCTGAC AGACAGCACC AAGAAGTAAT TGCAATTTAT CGGACACACC TTCTTAGTGC   180
TGCACAGGTA AAGAACTACT TCTCCTTTGG AAAGAATATT GCTTTAGAGA TAATAATTTT   240
TATTTTCAAA TAAATTTATG TGAAAGTAAT TG ATG TTT AAA GTA GCT GCA CCC   293
                               Met Phe Lys Val Ala Ala Pro
                               -25                      -20

CCT ATG CTT ATT TAW KAA ATA ATT ATG TTT CTT TTA ATC ATT GTT TGT   341
Pro Met Leu Ile Xaa Xaa Ile Ile Met Phe Leu Leu Ile Ile Val Cys
                               -15                      -10                      -5

GGA TCT CCC AGG CCG   356
Gly Ser Pro Arg Pro
1

```

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 228..322
id N29854
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..46)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 363..408
id N29854
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(44..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 315..364
id N29854
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(87..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 67..161
id T32629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..93)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 154..246
id T32629
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(87..181)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 230..324
id W61289
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(6..93)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 317..404
id W61289
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(87..181)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 232..326
id N53422
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(3..93)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 318..409
id N53422
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..181
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 78..172
id N50275
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..85
id N50275
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 64..126
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXMCLWSLRNLF/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:


```

AGCTATTTGG ATAGTGTAGC TTTAATGTGC TGCACATGAT ACTGGCAGCC CTAGAGTTCA    60
TAG ATG GAC TTT TGG GAC CCA GCA GTT TTT RAA ATG TGT TTA TGG AGT    108
  Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser
    -20                -15                -10

TTA AGA AAT TTA TTT TCC AGG TGC AGC CCC TGT CTA ACT GAA ATT TCT    156
Leu Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser
    -5                1                5                10

CTT CAC CTT GTA CAC TTG ACA GCT GAA AAA AAA CAA CAT GGG AGT AAT    204
Leu His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn
          15                20                25

AAT GGG TCG GCG
Asn Gly Ser Ala
          30

```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..114
id R56502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 162..258
id R56502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 119..162
id R56502

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 160..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq SVPLLSLSHSIGI/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

```

AGTGACCAAA TGACTTAACC ACAGATGGAG TGAAGACAGG GGTAAC TGCT TGGTCTGGTC   60
CCCAAGTAGAG CATTGCTCAC TATAAACCAC AAGCTGCTTC TAATTTATTT GAGRTGKTAW  120
TAAYCGTGGG CCTTKATATT CTGGTCTCTC TTGCTGCAA ATG AGT CCG GCA GGC   174
                               Met Ser Pro Ala Gly
                               -30
AAG CAC AAC TCA GAA AGC AAA TTC ACC TTC TTT GTA GCC CTT GAT GGG   222
Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe Val Ala Leu Asp Gly
          -25                      -20                      -15
TCG GTC CCC CTG TTG TCT CTT TCT CAT TCC ATA GGC ATT TCC CCC ACA   270
Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile Gly Ile Ser Pro Thr
          -10                      -5                      1
AGG
Arg..                                     273

```

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(78..160)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 149..231
id H15081
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(1..71)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 238..308

id H15081

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(2..71)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 234..303
id H16744
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(78..160)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 148..230
id R61691
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(2..72)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 236..306
id R61691
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(2..85)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 220..306
id H17833
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(109..160)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 148..199
id H17833
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 23..73

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq LVCVGLHTEGPNW/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

ATGTCGTGCTGT TGTGCTCTTAA CT ATG CAC TGG GCC CTT TGC GTC GCC TTG 52
Met His Trp Ala Leu Val Cys Val Gly Leu

-15

-10

| | |
|---|-----|
| CAT ACA GAG GGC CCC TGG GGT CGG CCC TCC GGC CTG GCC TCA GCC AGT | 100 |
| His Thr Glu Gly Pro Trp Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser | |
| -5 1 5 | |
| GGG ATG GAC AGG GCC AGG CAG GCC TCT GAA CTT CCA CCT CCT GGG GCC | 148 |
| Gly Met Asp Arg Ala Arg Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala | |
| 10 15 20 25 | |
| TCC CAG ACC CCC CAG | 163 |
| Ser Gln Thr Pro Gln | |
| 30 | |

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 155..325
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..58
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 170..340
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..62

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..35
id H17763
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 86..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 168..247
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 11..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..52
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 183..222
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 268..307
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 86..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 111..263
id AA084554
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 86..256
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 136..306
id R52491
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 20..235
(C) IDENTIFICATION METHOD: Von Heine matrix
(D) OTHER INFORMATION: score 3.5
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```

AGAGCTCGCT GTGGCCCGG ATG TTC GGT GCA GCT GCC AGA TCC GCT GAT CTA      52
               Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu
               -70      -65

GTG CTT CTC GAA AAA AAC CTT CAG GCG GCC CAT GGG TAT GCC CAA GAG      100
Val Leu Leu Glu Lys Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu
   -60      -55      -50

GAC AGA GAA CGA ATG CAC AGA DRT ATT GTC AGC CTT GSA CAG AAT CTC      148
Asp Arg Glu Arg Met His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu
   -45      -40      -35      -30

CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG CAA TGC TTC CTC      196
Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu
           -25      -20      -15

TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CCG GGA AAA AGA GTT      244
Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val
           -10      -5      1

CCA GCG CAC TTT
Pro Ala His Phe
      5

```

256

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..114
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..81
id AA094982
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..130

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..79
id T68050
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..84
id AA157180
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..81
id AA186993
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 43..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

| | |
|---|-----|
| AGCCGGAGCA AAGTTTCACT TATAGAAGGG AGAGGAGCGA AC ATG GCA GCG CGT | 54 |
| Met Ala Ala Arg | |
| -25 | |
| TGG CGG TTT TGG TGT GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC | 102 |
| Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val Ala Leu Leu Ile | |
| -20 -15 -10 | |
| GTT TGC GAC GTT CCC TCA GCC TCT GCC CGG | 132 |
| Val Cys Asp Val Pro Ser Ala Ser Ala Arg | |
| -5 1 | |

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..233
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 16..181
id W32979
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 316..394
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 260..338
id W32979
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..322
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 194..265
id W32979
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 107..293
id AA128556
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 145..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..94
id AA128556
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..391
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 104..234
id T20234
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 153..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98

region 6..91
id T20234
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 383..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 235..289
id T20234
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 115..238
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 65..188
id T32594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..318
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 201..263
id T32594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 52..115
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..64
id T32594
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 245..292
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLLQPSHIQEVWT/XY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```
ATCAGACGCC AGTATAAGCC TTGAGTCTC AATAGACTGC AATATCTTAT TGATTGGGGT   60
CGTGTGATC CTAGTCAACC TATTGACTTA ACCCAGCTTG TCAATGGGAG AGGTGTGACC  120
ATCCAGCCAC TTTAAAGGGA TTATGGTGTG CAGCTGGTTG AGGAGGGTGC TGACACCTTT  180
ACGGCAAAAG TTAATATTGA AGTACAGTTG GCTTCAGAAC TAGCTATTGC TGCCATTGAA  240
AAAA ATG GTG GTG TTS TTA CTA CAG CCT TCT ATG ATC CAA GAA GTC TGG   289
Met Val Val Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp
      -15              -10                      -5
```

| | |
|---|-----|
| ACA THG TAT GCA AAC CTG TTC CAT TCT TTC TTC GTG GAC AAC CCA TTC | 337 |
| Thr Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe | |
| 1 5 10 15 | |
| CAA AAA GAA TGC TTC CAC CAG AAG AAC TGG TAC CAT ATT ACA CTG ATG | 385 |
| Gln Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met | |
| 20 25 30 | |
| CAA AGA ACC GTG GGT ACC TGG CGG ATC CTG CCA AAT TTC CTG AAG CAC | 433 |
| Gln Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His | |
| 35 40 45 | |
| GAC | 436 |
| Asp | |

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 82..407
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 98.5
region 1..326
id HSARSE
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..171
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..84
id AAL60312
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 149..241
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LAVLLSLAPSASS/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

| | |
|---|-----|
| AAAAGCTGCGAA GTTAATCATTT CCCAGCTCAA AGCCTTGTCGC AASTGCTCTC TGCCTTCACG | 60 |
| CTTGCTTCCT TTGGGAGAGA ACCTTCCTCT TCTTGATCGG CATTTCAGGA AGGAGCCCAG | 120 |
| GRGCAGAGGA AGTAGAGAGA GAGRCAAC ATG TTA CAT CTG CAC CNT TCT TGT Met Leu His Leu His Xaa Ser Cys -30 -25 | 172 |
| TTG TGT TTC AGG AGC TGG CTG CCA GCG ATG CTC GCT GTA CTG CTA AGT Leu Cys Phe Arg Ser Trp Leu Pro Ala Met Leu Ala Val Leu Leu Ser -20 -15 -10 | 220 |
| TTG GCA CCA TCA GCT TCC AGC GAC ATT TCC GCC TCC CGA CCG AAC ATC Leu Ala Pro Ser Ala Ser Ser Asp Ile Ser Ala Ser Arg Pro Asn Ile -5 1 5 | 268 |
| CTT CTT CTG ATG GCG GAC CTT GGC ATT GGG GAC ATT GGC TGC TAT Leu Leu Leu Met Ala Asp Asp Leu Gly Ile Gly Asp Ile Gly Cys Tyr 10 15 20 25 | 316 |
| GGC AAC AAC ACC ATG AGG ACT CCG ARN ATT GAC CSC CTT GCA GAG GAC Gly Asn Asn Thr Met Arg Thr Pro Xaa Ile Asp Arg Leu Ala Glu Asp 30 35 40 | 364 |
| GGC GTG AAG CTG ACC CAA CAC ATC TCT GCC GCA TCT TTG TGC Gly Val Lys Leu Thr Gln His Ile Ser Ala Ala Ser Leu Cys 45 50 55 | 406 |

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
(B) TYPE: AMINO ACID
(C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 15.6
seq LLLLLLLRHGAQG/KP

(X1) SEQUENCE DESCRIPTION: SEQ ID NO: 3;;

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His
-20 -15 -10 -5
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14
seq LAMLALLSPLSLA/QY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu
-25                -20                -15                -10

Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro Xaa
               -5                1                5

Xaa Pro Glu Tyr Phe Gln Gln Pro
          10                15

```

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.3
seq HILFLLLPVAAA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

```

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
          -13                -10                -5

```

Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
 1 5 10
 Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
 15 20 25 30
 Leu Leu Ala Gly Leu Val Ala
 35

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.2
seq LALALSLAQPSA/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

Mét Ala Val Lys Leu Gly Thr Leu Leu Leu Ala Leu Ala Leu Gly Leu
 -20 -15 -10

Ala Gln Pro Ala Ser Ala Arg Arg Lys Leu Leu Val Phe Leu Leu
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.9

seq LVLEFLLSPVEA/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu Ser
-20          -15          -10          -5
Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu
          1          5          10
Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu Val
          15          20          25
Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp Glu
          30          35          40
Glu Glu Thr Thr Phe Arg Met Glu Ser Gly
          45          50

```

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.3
seq PLLSSLLGGSQA/MD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
-15          -10          -5
Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
          1          5          10          15
Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro Thr
          20          25          30
Arg Leu Asp Arg Val Tyr Pro Ser Arg
          35          40

```

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LWLLFFLVTAIHA/EL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

```

Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala Glu Leu
      -10                      -5                      1
Cys Gln Pro Gly Ala Glu Asn Ala Phe Lys Val Arg Leu Ser Ile Arg
      5                      10                      15
Thr Ala Leu Gly Asp Lys Ala Tyr Ala Trp Asp Thr Asn Glu Glu Tyr
      20                      25                      30
Leu Phe Lys Ala Met Val Ala Phe Ser Met Arg Lys Val Pro Asn Arg
      35                      40                      45                      50
Glu Ala Thr Glu Ile Ser His Val Leu Leu Cys Asn Val Thr Gln Arg
      55                      60                      65
Val Ser Phe Trp Phe Val Val Thr Asp Pro Ser Lys Asn His Thr Leu
      70                      75                      80
Pro Ala Val Glu Val Gln Ser Ala Ile Arg Met Asn Lys Asn Arg Ile
      85                      90                      95
Asn Asn Ala Phe Phe Leu Asn Asp Gln Thr Leu Gln Phe Leu Lys Ile
      100                     105                     110
Pro Ser Thr Leu Ala Pro Thr Arg
      115                     120

```

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq LPLLCIFLQGATA/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```

Met Ala Gly Ser Pro Ser Arg Ala Ala Gly Arg Arg Leu Gln Leu Pro
  -25                               -20                -15

Leu Leu Cys Leu Phe Leu Gln Gly Ala Thr Ala Val Leu Phe Ala Val
  -10                               -5                1                5

Phe Val Arg Tyr Asn His Lys Thr Asp Ala Ala Leu Trp Xaa Arg Lys
          10                15                20

Leu Gly

```

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.6
seq ALALLLVLP LLWP/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

Met Lys Trp Pro Trp Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Val
  -35                               -30                -25

Leu Ser Pro Pro Cys Ser Gly Pro Xaa Leu Ala Leu Ala Leu Leu
  -20                               -15                -10

Val Leu Pro Leu Leu Trp Pro Cys Ser Val Phe Gly His Ala Leu Cys
  -5                1

Xaa Pro Ser Pro Ala Arg Arg

```


10

15

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10
seq PLLGLLLSLPAGA/DV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```

Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu Leu
-20                               -15                               -10

Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys Gly Glu
-5                               1                               5

Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala Asp Ile Pro
10                               15                               20                               25

Tyr Gln Glu Ile Ala Xaa Glu His Leu Arg Ile Cys Pro Gln Glu Tyr
30                               35                               40

Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu Ser Gln Gln Ser Lys
45                               50                               55

Leu Glu Phe Glu Asn Leu Val Glu Glu Thr Ser His Phe Val Arg Thr
60                               65                               70

Thr Phe Val Ser Arg His Lys Lys Phe Asp Gly Arg
75                               80                               85

```

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -28...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10
 seq LWLSLLVPSC/LCA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

```

Met Leu Leu His Trp Val Arg Ser Gln Xaa Xaa Ser Asp Xaa Lys Leu
   -25                               -20                -15

Trp Leu Ser Leu Leu Val Pro Ser Cys Leu Cys Ala Ser Pro Trp Pro
   -10                               -5                      1

Leu Pro Ser Leu Pro Leu Leu Leu Pro Pro Ser Leu Leu Ser Leu Leu
   5                               10                15                20

```

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -34...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.6
 seq LLLFSLLVSPPTC/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

```

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
   -30                               -25                -20

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
   -15                               -10                -5

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
   1                               5                10

Trp Xaa Thr Pro Pro Thr Arg Trp
   15                               20

```

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq AMWWLLNGVLQA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

```

Met Pro Gly Pro Arg Val Trp Gly Lys Tyr Leu Trp Arg Ser Pro His
-35                               -30                               -25                               -20

Ser Lys Gly Cys Pro Gly Ala Met Trp Trp Leu Leu Leu Trp Gly Val
-15                               -10                               -5

Leu Gln Ala Trp Pro Xaa Pro Gly Leu Arg Pro Leu Gly Pro Arg Ala
1                               5                               10

Thr Pro Ala Ala Asp Ile Pro Arg Val Pro Arg Ala Val Trp Gln Arg
15                               20                               25

Pro Arg Glu Gln His Gly His Gln Gly Ser Arg Gly Leu Cys Cys Glu
30                               35                               40                               45

Ala Arg Leu Pro Gly Leu Arg Pro Gly Ala Val Pro Gly Leu Cys Arg
50                               55                               60

Gly Leu Xaa Xaa Asn Leu Ile Arg Arg Phe Gly Ser Lys Pro Val Leu
65                               70                               75

Trp Ser Ala Arg Leu Pro Ser Gly Gln Ala Pro Trp Ser Glu Gly
80                               85                               90

```

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -37...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq LLAVLLASWRLWA/IK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

```

Met Cys Gly Pro Ala Met Phe Pro Ala Gly Pro Pro Trp Pro Arg Val
-35                                -30                    -25

Arg Val Val Gln Val Leu Trp Ala Leu Leu Ala Val Leu Leu Ala Ser
-20                                -15                    -10

Trp Arg Leu Trp Ala Ile Lys Asp Phe Gln Glu Cys Thr Trp Gln Val
-5                                1                      5              10

Val Leu Asn Glu Phe Lys Arg Val Gly Glu Ser Gly Val Ser Asp Xaa
15                                20                    25

Ser Leu Ser Lys Ser Pro Gly
30

```

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -55...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq SLLLLSTALNILA/CQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

```

Met His Arg Arg Lys Leu Pro Leu Thr Asn Lys Arg Gln Leu Gln Lys
-55                                -50                    -45                    -40

Xaa Leu Ser Lys Phe Ile Phe Ser Asp Glu Leu Phe Arg Asn Ile Leu
-35                                -30                    -25

Phe Ser Leu Arg Thr Leu Arg Met Ile Leu Ser Leu Leu Leu Ser

```

-20

-15

-10

Thr Ala Leu Asn Ile Leu Ala Cys Gln Ile Asn Glu Leu Gly
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heljne matrix
- (D) OTHER INFORMATION: score 8.3
seq VSALLMAWFGVLS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val Leu
-15 -10 -5

Ser Cys Val Gln Ala Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heljne matrix
- (D) OTHER INFORMATION: score 8.1
seq LCLVCLLVHTAFR/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

Met Gln Leu Pro Leu Ala Leu Cys Leu Val Cys Leu Leu Val His Thr
-15 -10 -5

Ala Phe Arg Val Val Glu Gly Gln Gly Trp Gln Ala Phe Lys Asn Asp
1 5 10

Ala Thr Glu Ile Ile Pro Glu Leu Gly Glu Tyr Pro Glu Pro Pro Pro
15 20 25

Glu Arg
30

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -31..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8
seq ILLCSVAVXLSPS/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3.5:

```
Met Leu Cys Ile His Xaa Xaa Arg Ile Ile Gln Asp Ser Phe Ile Ala  
-30 -25 -20
```



```
Leu Lys Ile Leu Leu Cys Ser Val Ala Val Xaa Leu Ser Pro Ser Glu  
-15 -10 -5 1
```



```
Pro Leu Ala Pro  
5
```

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -38...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LPFLSLFWPWAPG/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Gly Gly Phe Phe Pro Pro Thr Glu Val Arg Glu Val Cys Ala Asn
-35 -30 -25
Gln Gly Ala Ala His Asn Arg Asp Arg Leu Pro Phe Leu Ser Leu Phe
-20 -15 -10
Trp Pro Trp Ala Pro Gly Ala Val Ser Val Gly Gln Ala Arg Tyr Arg
-5 1 5 10
Thr Pro Thr Thr Xaa Ala Pro Ser Ala Ser Val Pro Trp Pro Arg Ala
15 20 25
Gly Thr Cys Arg Thr Pro Thr
30

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -30...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq HLWILLLSFCWM/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Lys Leu Phe Tyr Asn Gln Leu Val Ser Glu Thr Lys His Asp Phe
-30 -25 -20 -15
Ala His Leu Trp Ile Leu Leu Leu Phe Ser Phe Cys Trp Met Ser Arg
-10 -5 1
Ser Phe Phe Phe Phe
5

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLFFHILFHSCFS/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Pro Ser Glu Ser Pro Pro Leu Leu Phe Phe His Ile Leu Phe His
-20 -15 -10 -5
Ser Cys Phe Ser His Leu Leu
1

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -68...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLCSALAWQQSLG/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly Gly Val Lys Ile Tyr
-65 -60 -55
Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala Met Met Asn Ser Ile

-50 -45 -40
 Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu Leu Glu Ser Pro Thr
 -35 -30 -25
 Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser Ala Leu Ala Trp Gln
 -20 -15 -10 -5
 Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly Val Ser Glu Lys Ala
 1 5 10
 Glu Val Gln Leu Ser Cys Cys Cys Ala Cys His Ser Lys Asp Phe Thr
 15 20 25
 Asn Asn Asp Met Asn Gln Gly Thr Ser Arg His Phe Asn Tyr Pro Ser
 30 35 40
 Thr Pro Arg
 45

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq FVRFLGHVSCQLQS/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

Met Ala Leu Phe Leu Glu Leu Phe Leu Asn Ser Tyr Ser Leu Leu Phe
 -25 -20 -15
 Val Arg Phe Leu Gly Phe Val Ser Cys Leu Gln Ser Asp Pro Ile Cys
 -10 -5 1
 Ser Phe Phe Phe Phe
 5

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq LMAGSSLSAGVSG/ED

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

Met Asn Glu Asp Glu Lys Glu Met Lys Glu Ile Leu Met Ala Gly Ser
-20 -15 -10

Ser Leu Ser Ala Gly Val Ser Gly Glu Asp Lys Thr Glu Ile Leu Asn
-5 1 5

Pro Thr Pro Xaa Met Ala Lys Ser Leu Thr Ile Asp Cys Leu Glu Leu
10 15 20

Ala Leu Pro Pro Glu Leu Ala Phe Gln Leu Asn Glu Leu Phe Gly Pro
25 30 35 40

Val Gly Ile Asp Ser Gly Ser Leu
45

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.8
seq IIPLIKKLSLCLC/LW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

Met Gly Ser Phe Leu Leu Gly Gly Ile Ile Pro Leu Ile Xaa Xaa Leu

-20

-15

-10

Ser Leu Cys Leu Cys Leu Trp Trp Arg Ile Ile
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq VCLLCSGCSCAWS/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Leu Gln Val Ala Thr Thr Asn Tyr Leu Glu Leu Ala Arg Glu Val
-30 -25 -20

Lys Pro Val Cys Leu Leu Cys Ser Gly Cys Ser Cys Ala Trp Ser Val
-15 -10 -5

Gly Cys Val Xaa Glu Ser Glu Ser Glu
5 10

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7

seq PFFLALDFPKSTS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Phe Cys Leu Ala Pro Phe Phe Leu Ala Leu Cys Phe Pro Lys Ser
 -15 -10 -5
 Thr Ser Gln Pro Gln Arg
 1

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.5
seq QCLLCCTISPPVFC/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ser Glu Ser Arg Phe Gln Pro Gln Asn Gln Gly Gly Ser Leu Gln
 -30 -25 -20
 Leu Pro Leu Gln Cys Leu Leu Cys Cys Ile Ser Pro Pro Val Phe Cys
 -15 -10 -5
 Glu Gly Asn Trp Leu Ser Tyr Phe Tyr Val Leu Pro Gly Phe Val Cys
 1 5 10 15
 Glu Leu His Lys Leu Gly Ile Ser Cys Leu Ile Pro Leu Phe Ser Val
 20 25 30
 Ser Pro Leu Ala Ala Trp Met Val
 35 40

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -23...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.3
 seq SSCLLEHLSSQ/FS-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

Met Pro Lys His Cys His Ser Phe Ile Thr Ser Ser Cys Leu Leu Gly
 -20 -15 -10
 Leu Leu His Leu Ser Ser Gln Phe Ser Cys Pro Gly Arg Lys Leu His
 -5 1 5
 Pro Ala Gln Arg His Thr Glu Ala Glu Thr Gln Gly Arg Pro Leu Ser
 10 15 20 25
 Asp Arg

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -19...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq FIXFPFLFPFSFS/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

Met Cys Leu Leu Phe Xaa Phe Ile Xaa Phe Pro Phe Leu Phe Pro Phe
 -15 -10 -5
 Ser Phe Ser Gln Thr Phe Ser Phe Ser Gln His Trp Asn Thr Gly Gly
 1 5 10
 Ser His Pro Glu Glu Leu Glu Arg Pro Gly Ala His Pro Arg Leu Lys
 15 20 25

Ala Arg Pro Gln Pro Pro Leu Phe His Pro Phe Ile Ser Ser
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLVASGRAGCVSA/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

Met Ala Ser Glu Arg Xaa Pro Asn Arg Pro Xaa Cys Leu Leu Val Ala
 -25 -20 -15 -10
 Ser Gly Xaa Ala Glu Gly Val Ser Ala Gln Ser Phe Leu Xaa Cys Phe
 -5 1 5
 Thr Met Ala Ser Thr Xaa Phe Asn Leu Gln Val Ala Xaa Pro Gly Gly
 10 15 20
 Lys Ala Met Glu Phe Val Asp Val Thr Xaa Ser Asn Ala Arg Trp Val
 25 30 35
 Gln Asp
 40

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -25..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LAFQLVFLRATSG/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

```

Met Phe Pro Asp Tyr Lys Leu Gly Gly Ser Tyr Leu Leu Ala Phe Gln
-25          -20          -15          -10
Leu Val Phe Leu Arg Ala Thr Ser Gly Ser Cys Ser Lys Tyr Arg Arg
          -5              1              5
His Leu His Asn Ile Asn Val Arg Pro Gly Leu Val Arg Leu Leu Gly
          10              15              20
Ser Cys Ile Gln Lys Gln Pro Gly
          25              30

```

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -25..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LLLXLKLLLIAE/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

```

Met Arg Arg Ile Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa
-25          -20          -15          -10
Leu Xaa Leu Leu Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser
          -5              1              5
Leu Cys Phe Asn Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro
          10              15              20
Trp Cys Glu Ala His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr
          25              30              35
Asn Ser Asp Asn Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys
          40              45              50              55

```

Val Tyr Ala Thr Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu
60 65 70
Val Gly Arg Asp Leu Arg Met Leu Leu Cys Asp Ile Lys
75 80

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq TFLLLXNAGRS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

Met Thr Phe Leu Leu Leu Leu Phe Xaa Asn Ala Gly Arg Ser Leu Arg
-10 -5 1

Met Cys

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq EMFLVLLVTGVHS/NK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met Phe
 -25 -20 -15
 Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr Ala Lys
 -10 -5 1 5
 Lys Ile Lys Arg Pro Gly
 10

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq ISLLFIFFSIANS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Ser Ser Pro Leu Leu Val Glu Gln Ser Ser Thr Lys Ser Pro Lys
 -40 -35 -30 -25
 Ser Trp Ser Trp Ser Phe Leu Ala Phe Ser Cys Ile Ser Leu Leu Phe
 -20 -15 -10
 Ile Phe Phe Ser Ile Ala Asn Ser Ser Pro Cys Gly
 -5 1

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq IPLLLLFFHLSFL/NS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Tyr Leu Phe Cys Leu Phe Ser Val Ser Lys Thr Ile Pro Leu Leu
-25 -20 -15 -10

Leu Leu Phe Phe His Leu Ser Phe Leu Asn Ser Leu
 -5 1

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 43 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.9
seq CLLILKFLSPAST/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

```
Met Ile Val Cys Leu Leu Ile Leu Lys Phe Leu Ser Pro Ala Glu Thr
  -15                      -10
Ser Ile Leu Ser Ser Ile Ala Thr Tyr Gly Ala Phe Tyr Phe Ile Val
  1                      5                      10                      15
Pro Leu Glu Val Ser Gln Ile Leu Gln Thr Gln
      20                      25
```

2: INFORMATION FOR SEQ ID NO: 344:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq LILCFILHHT/HT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

Met Asp Lys Ser Ile Lys Ser Ser Ile Ile Trp Ser Leu Ile Leu Cys
-25 -20 -15 -10

Phe Leu Phe Ile Leu His Thr His Thr His Thr His Thr His
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
                        seq IFOLLXXXSNQ/LP
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

Met Phe Phe Ile Phe Ile Asn Gly Phe Thr Leu Leu Leu Met Thr Leu
-35 -30 -25

Ala Met Lys Pro Arg His Pro Ile Phe Asp Leu Leu Leu Leu Xaa
-20 -15 -10 -5

Xaa Ser Asn Gln Leu Pro Val Thr Gly
 :
 5

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LWPFLTWINPALS/IC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Cys Pro Ser Leu Glu Glu Ala Pro Ser Val Lys Gly Thr Leu Pro
-60 -55 -50 -45
Cys Ser Gly Gln Gln Gln Pro Phe Pro Phe Gly Ala Ser Asn Ile Pro
-40 -35 -30
Leu Leu Leu Gly Arg Ser Arg Lys Val Ala Arg Gly Ala Pro Val Leu
-25 -20 -15
Trp Pro Phe Leu Thr Trp Ile Asn Pro Ala Leu Ser Ile Cys Asp Pro
-10 -5 1
Leu Gly Ser Cys Gly Trp Gln
5 10

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSALWFCHPCCL/CC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Leu Gln Asp Leu Leu Ser Ala Leu Trp Phe Cys His Pro Cys Cys
 -15 -10 -5
 Leu Cys Cys Gly Leu Cys Trp Leu Gly Val Asp Ala Gly Cys Ser Gln
 1 5 10 15
 Gly Gly Ser Gly Cys Pro
 20

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LLSLAAYLSGPHQ/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Met Asp Leu Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly
 -15 -10 -5
 Pro His Gln Glu Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn
 1 5 10
 Leu Pro Lys Pro Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp
 15 20 25
 Lys Ala Glu Gln Glu Arg Val Glu Val Glu
 30 35

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -19...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq LLPGLPLVRTSFS/HF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Glu Met Pro Pro Cys Leu Leu Pro Gly Leu Pro Leu Val Arg Thr
-15 -10 -5

Ser Phe Ser His Phe Phe Ser Leu Ser Gly Gly Thr Thr Thr Ala Arg
1 5 10

Gly

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -25...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq GLANLHVTRGVXG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Thr Val Glu Leu Trp Leu Arg Leu Arg Gly Lys Gly Leu Ala Met
-25 -20 -15 -10

Leu His Val Thr Arg Gly Val Xaa Gly Ser Arg Val Arg Val Xaa Xaa
-5 1 5

Xaa Leu Pro Ala Leu Leu Gly Xaa Pro Arg Ala Leu Ser Ser Xaa Ala
10 15 20

Ala Lys Met Gly Xaa Tyr Arg Xaa Met Trp
25 30

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq LLILLCSSPPDRV/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

```

Met Ser Ile Glu Asp Phe Val Asn Arg Ser Ile Leu Leu Ile Leu Leu
      -20                      -15                      -10
Cys Ser Ser Pro Pro Asp Arg Val Ser Tyr Arg Ala Lys Val Leu His
      -5                      1                      5
Ser Leu Leu Gln Leu Pro Ala Gln
      10                      15

```

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq FALLFLFLVPPVPG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

```

Met Arg Ile His Tyr Leu Leu Phe Ala Leu Leu Phe Leu Phe Leu Val
-20                      -15                      -10                      -5
Pro Val Pro Gly His Gly Gly Ile Ile Asn Thr Leu Gln Lys Tyr Xaa

```


(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -18...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq GLALVAGTPPSRS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Met Gly Asn Pro Gly Leu Ala Leu Val Ala Gly Thr Pro Pro Ser
 -15 -10 -5

Arg Ser Cys Pro Gln Ala Asn Ser Gln Thr Arg
 1 5

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -39...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq PCVSLWAPRXFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu Met
 -35 -30 -25

Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu Trp
 -20 -15 -10

Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr Leu
 -5 1 5 10

Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys Asp
 15 20 25

Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His Cys
 30 35 40

Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr
 45 50

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SLLXLRASQLSEG/DT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly His Val Val Phe Gly Asp Ile Lys Asn Ser Leu Leu Xaa Leu
-20 -15 -10
Arg Ala Ser Gln Leu Ser Glu Gly Asp Thr Xaa Xaa Xaa Xaa Cys Pro
-5 1 5
Xaa Met Xaa Arg Gly Lys His Ile Ser Tyr
10 15

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -91...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq FLSLLXSVSETPG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ala Gly Gly Arg Arg Asp Tyr Ser Gln Leu Phe Gly Arg Gly Pro
-80 -75 -70

Gly Arg Leu Ser Arg Ala Arg Ala Ser Val Val A : Trp Ser Pro Arg
 -65 -60 -55 -50
 Ala Thr Ala Cys Pro Ala Pro Pro Ser Leu Pro Asp Leu Lys Arg Gln
 -45 -40 -35
 Glu Leu Val Ser Arg Ile Glu Cys Gly Cys Arg Gly Pro Val Gly Ala
 -30 -25 -20
 Thr Ala Asp Phe Phe Leu Ser Leu Leu Xaa Ser Val Ser Glu Thr Pro
 -15 -10 -5
 Gly Ser Leu Arg Xaa Asn Asp Leu Phe Phe Val Ser Gln Leu Ile Trp
 1 5 10 15
 Gly Arg

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LWCFHSFISFSLSS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Phe Trp Xaa Gly Ser Leu Trp Cys Phe His Ser Phe Ile Ser Phe
 -15 -10 -5
 Ser Leu Ser Ser Ser Arg
 1

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -36..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq FLLTFFSYSLHA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

```

Met Ala Trp Pro Asn Val Phe Gln Xaa Gly Ser Leu Leu Ser Gln Phe
-35                      -30                      -25

Xaa Xaa His His Val Val Val Phe Leu Leu Thr Phe Phe Ser Tyr Ser
-20                      -15                      -10                      -5

Leu Leu His Ala Ser Arg Lys Thr Phe Xaa Asn Val Lys Val Ser Ile
                      1                      5                      10

Ser Glu Gln Trp Thr Pro Ser Ala Phe Asn Thr Ser Val Glu Leu Pro
                      15                      20                      25

Val Glu Ile Trp Ser Ser Xaa His Leu Phe Pro Ser Ala Glu
30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq WILAVGLSLPSSS/XI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

```

Met Ile Leu Arg Asn Leu Trp Ile Leu Ala Val Gly Leu Ser Leu Pro
-15                      -10                      -5

Ser Ser Ser Xaa Ile Lys Phe His Phe Ser Leu Tyr Ser
1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LCGLLHLWLKVS/LK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Thr Val Asn Asp Val Arg Phe Tyr Arg Asn Val Arg Ser Asn
-35 -30 -25 -20
His Phe Pro Phe Val Arg Leu Cys Gly Leu Leu His Leu Trp Leu Lys
-15 -10 -5
Val Phe Ser Leu Lys Gln Leu Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq LFLNLCILAXPFS/KQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Asn Leu Lys Pro Gly Leu Pro Cys Asn Leu Phe Leu Asn Leu Cys
 -20 -15 -10
 Ile Leu Ala Xaa Pro Phe Ser Lys Gln Ile Ile Glu Leu Leu Glu Tyr
 -5 1 5
 Val Ser Tyr His Pro Cys Val Leu Val Tyr Ser Glu Tyr Xaa Asn Ile
 10 15 20 25
 Ser Ile Val Tyr Thr Leu
 30

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq VVLAVGLLNVSMA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Met Gln Gly Glu Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr
 -40 -35 -30 -25
 Ile Lys Met Arg Lys Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp
 -20 -15 -10
 Gly Leu Leu Asn Val Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr
 -5 1 5
 Gly Lys Leu Ile Ser Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp
 10 15 20
 Tyr Xaa Glu Leu Ala Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe
 25 30 35 40
 Asp Phe Trp Arg Tyr Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val
 45 50 55
 Val Ser Pro Gly Arg
 60

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq PXXLL LAHITQS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Met Asn Gln Thr His Pro Xaa Xaa Leu Leu Ile Leu Ala His Ile
 -15 -10 -5
Thr Gln Ser Cys Pro Trp Ala His Val Gly Ala Ala Pro Ser Ala Leu
 1 5 10
Leu Ile His Arg Trp Glu Leu Arg Gly Cys Ser Tyr Leu Lys Leu Phe
 15 20 25
Leu Val Met Val Leu Ile Phe Glu Met Leu
 30 35

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq GLVLLLSLAELF/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Gly Leu Pro Glu Arg Arg Gly Leu Val Leu Leu Ser Leu Ala
 -20 -15 -10 -5
 Glu Ile Leu Phe Lys Ile Met Ile Leu Glu Gly Gly Gly Val Met Asn
 1 5 10
 Leu Asn Pro Gly Asn Asn Leu Leu His Gln Pro Pro Ala Trp Thr Asp
 15 20 25
 Ser Tyr Ser Thr Cys Asn Val Ser Ser Gly Phe Phe Gly Gly Gln Trp
 30 35 40
 His Glu Ile His Pro Gln Tyr Trp Thr Lys Tyr Gln Val Trp Glu Trp
 45 50 55 60
 Leu Gln His Leu Leu Asp Thr Asn Gln Leu Asp Ala Asn Cys Ile Pro
 65 70 75
 Phe Gln Glu Phe Asp Ile Asn Gly Glu Xaa Arg
 80 85

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq LCWALLYNCFSSS/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Trp Gly Leu Glu Glu Asp Arg Ser Tyr Gln Gly Leu Arg Pro Leu
 -25 -20 -15
 Cys Trp Ala Leu Leu Tyr Asn Cys Phe Ser Ser Ser Cys Val Pro Val
 -10 -5 1
 Ala Leu Val
 5

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -85...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ALLASLGIAFSRS/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

```

Met Leu Cys Arg Asp Gly Ser Ala Cys Val Pro Arg Ser Arg Arg Leu
-35                               -80                               -75                               -70
Pro Leu Pro Ala Ala Val Arg Ala His Gly Pro Met Ala Asp Xaa Xaa
                               -65                               -60                               -55
Asp Ser Ala Arg Gly Cys Val Val Phe Glu Asp Val Phe Val Tyr Phe
                               -50                               -45                               -40
Ser Arg Glu Glu Trp Glu Leu Leu Asp Asp Ala Gln Arg Leu Leu Tyr
                               -35                               -30                               -25
His Asp Val Met Leu Glu Asn Phe Ala Leu Leu Ala Ser Leu Gly Ile
                               -20                               -15                               -10
Ala Phe Ser Arg Ser Arg Ala Val Met Lys Leu
-5                               1                               5

```

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.7
seq FLCFLNLTSHLSG/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

```

Met Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
-55                      -50                      -45
Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
-40                      -35                      -30                      -25
Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
-20                      -15                      -10
Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
-5                      1                      5
Arg Arg Gly
10

```

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -38..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq LAFLSCLAFLVLD/TQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

```

Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser Val Ala
-35                      -30                      -25
Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser Cys Leu
-20                      -15                      -10
Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly Thr Arg
-5                      1                      5                      10
Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala Val Leu Trp
15                      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq DHLFLILFPRSCSS/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

```

Met Ser Asn Lys Tyr Ile Lys Pro Ser Met Ser Pro Gly Asn Thr Asp
      -25                      -20                      -15
His Leu Phe Leu Leu Phe Pro Arg Ser Cys Ser Ser Leu Val
      -10                      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq FFFFLFILPPKPP/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

```

Met Val Glu Leu Lys Gln Leu Gly Pro Arg Ser Phe Phe Phe Phe Leu
      -20                      -15                      -10
Phe Leu Leu Pro Pro Xaa Pro Pro Thr Gly
      -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LILPALFFFLHC/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Pro Tyr Val Thr Ile Pro Tyr Ile Ile Val Tyr Ser Leu Ile Leu
-25 -20 -15
Pro Ala Leu Phe Phe Phe Pro Leu His Cys Thr Phe His Gly Leu Thr
-10 -5 1 5
Tyr Tyr Ile Ser Cys Val Cys Ser Leu Ser Leu Pro Thr
10 15

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LLLCNLPHSVLS/NW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

Met Pro Pro Leu Ala Ala Val Met Gly Ser Leu Pro Leu Leu Cys

-25

-20

-15

-10

Met Asp Leu Pro His Ser Val Leu Ser Asn Trp
-5 1

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq EFLFLGFPNSNSWP/HR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Leu Gln Ile Pro Glu Arg Arg Glu Phe Leu Phe Leu Gly Phe Pro
-20 -15 -10
Ser Asn Ser Trp Pro His Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq FLITLFCCCVVVG/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Phe Phe Val His Phe Leu Ile Thr Leu Phe Cys Cys Cys Val Val
 -15 -10 -5
 Val Gly Phe Phe Gly His Asp His Ser Phe Ile Ser Gln Phe Ile Leu
 1 5 10
 Val Thr Trp Ala Arg Ala Gly
 15 20

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq CLLHLRCLQLYWA/AR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

Met Ala Cys Phe Gly Glu Lys Arg His Ala Lys Ser Cys Leu Leu His
 -25 -20 -15 -10
 Leu Arg Cys Leu Gln Leu Tyr Trp Ala Ala Arg
 -5 1

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.4
seq PLSIALQSSCCLC/LT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

Met Val Asp Arg Asp Glu Asn Ile Leu Leu Lys Gln Ile Tyr Ser Pro
-25 -20 -15
Leu Ser Leu Ala Leu Gln Ser Ser Cys Cys Leu Cys Leu Thr Ser Cys
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq VSVSLCVCDCVRG/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Lys Val Lys Pro Pro Phe Val Ser Val Ser Leu Cys Val Cys Asp
-20 -15 -10 -5
Cys Val Arg Gly Ser Thr Leu Thr Trp Asn Arg Leu Leu Arg Val Gly
1 5 10

Gly

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq ILLTSCFYTLVSS/TF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

```

Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala Ser Leu
  -35                      -30                      -25
Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr Ser Cys
  -20                      -15                      -10
Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser Ser Leu
  -5                      1                      5
Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys Thr Phe
  10                      15                      20                      25
Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile Asn Phe
  30                      35..                      40
Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu Phe Leu
  45                      50                      55
Ala Val Pro Arg
  60

```

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq SFLCN:LVSLSLSL/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

```

Met Gly Gly Gly Ile Ala Glu Ser Phe Leu Cys Asn Phe Leu Val Ser
-20                      -15                      -10                      -5
Leu Ser Leu Ser Phe Leu His Gly Arg

```


Met Glu Tyr Leu Phe Gln Gln Pro Gly His Ser Arg Gly Glu Ala Arg
 -35 -30 -25
 Ala Ala Ala Ala Ser Leu Glu Thr Leu Ser Ser Leu Trp Phe Leu Pro
 -20 -15 -10
 Leu Pro Thr His Val Tyr Thr His Thr His Ala Asn
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq SSMLTILSFIFA/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Val Ser Ser Met Leu Ile Thr Ile Leu Ser Phe Ile Phe Ala Leu
 -15 -10 -5 1
 Gly Tyr His Thr Ala Ser Tyr Pro Val Ser Leu His Pro Leu Ser Phe
 5 10 15
 Phe Leu His
 20

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -18..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.3
 seq MNLVSALASSAXG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Pro Leu Phe Thr Met Asn Leu Val Ser Ala Leu Ala Ser Ser Ala
 -15 -10 -5

Xaa Gly Gln Arg Gly Ala Gly Pro Ala Leu Trp His Leu Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: -39..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.2
 seq LILLHCSIRVFF/FF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

Met Ile Cys Lys His Tyr Cys Ile Lys Lys Asn Asn Leu Asp Tyr Leu
 -35 -30 -25

Asn Arg Met Val Tyr Ser Ala Gln Leu Lys Leu Ile Leu Leu His
 -20 -15 -10

Cys Ser Ile Arg Val Phe Phe Phe Phe
 -5 1

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -53..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq SFLLQLIHEDKA/IQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

```

Met Lys Ile Pro Val Trp His Lys Thr Cys Phe Leu Lys Ser Glu Ser
  -50                      -45                      -40
Phe Ser Pro Asp Asn Leu Ser Val Ser Leu Pro Cys Arg Pro Ser Gln
  -35                      -30                      -25
Val Pro Ser Gln Gly Gln Gly Lys Ser Phe Leu Leu Gln Leu Ile
  -20                      -15                      -10
His Glu Asp Lys Ala Ile Gln Asn Glu Ala Ile Phe Gln Pro Ser Leu
  -5                      1                      5                      10
Gln Leu

```

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq FGCTFVAFXPAFA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Xaa Pro
  -15                      -10                      -5
Ala Phe Ala Leu Ser Leu Ile Thr Val Ala Gly Asp Arg Gly
  1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LWSSCWLAPLADG/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Val Gly Gly Leu Asp Pro Pro Gly Arg Arg Arg Phe Gln Lys Gly
 -30 -25 -20

Phe Asp Trp Arg Asn Leu Trp Ser Ser Cys Trp Leu Ala Pro Leu Ala
 -15 -10 -5

Asp Gly Met Leu Arg Tyr Met Gly Gln Xaa Gln Arg Xaa Ala Ser Asn
 1 5 10

Pro Glu Gly Ser Thr Leu Glu Ala Arg Pro Pro Ala Pro Xaa Ala Ser
15 20 25 30

Val Ser Pro Ser Val Xaa Xaa Pro His Arg Pro Trp Ala Ala Lys Met
 35 40 45

Glu Thr Val Ser Pro Ala Thr Ser Xaa Ile Ala Gly Gly
 50 55

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq SLLVVSCFYQISG/RW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ser Lys Met Pro Val Phe Ala Ser Leu Leu Val Val Ser Cys Phe
-20 -15 -10

Tyr Gln Ile Ser Gly Arg Trp
-5 1

(2) INFORMATION FOR SEQ ID NO: 390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq VTQLLPFSSPDSA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Xaa Val Thr Gln Leu Leu Pro Phe Ser Ser Pro Asp Ser Ala Gly
-15 -10 -5 1

Pro Phe Leu Ser Pro Phe Ser
5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq SFHFLPWALGAMA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

```

Met Gly Lys Ala Trp Gln Glu Met Arg Val Glu Trp Gly Ala Asp Lys
   -30                               -25               -20

Gly Asn Val Arg Ser Ser Phe His Phe Leu Pro Trp Ala Leu Gly Ala
   -15                               -10               -5

Met Ala Ser Ser Glu Gln Gly Lys Glu Arg Ser Asn Leu Cys Phe Arg
      1                               5               10

Lys Thr Pro Leu Ala Ile Thr Gly Arg Gly Ile Ala Arg Arg Pro Gly
   15                               20               25               30

Gly Gly Trp Met Gly Met Trp Val
      35

```

(2) INFORMATION FOR SEQ ID NO: 392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq VIRLSQFLLKCWP/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```

Met Lys Val Met Met Arg Lys Arg Lys Lys Lys Asp Gln Cys Leu Pro
   -45                               -40               -35

Gly Ile Cys Arg Ser Leu Lys Arg Arg Lys Ser Pro Arg Ser Pro Gly
   -30                               -25               -20

Met Lys Val Ile Arg Leu Ser Gln Phe Leu Leu Lys Cys Trp Pro Arg
   -15                               -10               -5               1

Trp Ser Leu Thr Ala Ala Thr

```

(2) INFORMATION FOR SEQ ID NO: 393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SFSIXTLLWGLNC/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe Lys Pro Leu Leu
-35                               -30                   -25

Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa Thr Leu Leu Trp
-20                               -15                   -10                   -5

Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu Arg Ile Val Xaa
                               1                   5                   10

Ser Tyr Ser Ser Gly Tyr
15

```

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5

seq RLLLILSGCLVYG/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val Gly Pro Gly
 -40 -35 -30

Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg Leu Leu Leu
 -25 -20 -15 -10

Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr Asp Val Asn
 -5 1 5

Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg Ala Ser Leu
 10 15 20

Gly

(2) INFORMATION FOR SEQ ID NO: 395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq PLLSCSCPPPLLG/EG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Glu Met Thr Gly Val Trp Gln Cys Gln Ala Glu Ala Val Lys
 -30 -25 -20

Gly Leu Pro Pro Leu Leu Ser Cys Ser Cys Pro Pro Pro Leu Leu Gly
 -15 -10 -5

Glu Gly His Ala Gln Ala Ser Pro Leu Ala Gln Glu Glu Asp Lys Lys
 1 5 10 15

His Thr Glu Gln Thr Gln Ala Thr Ser Pro Thr Gln Pro
 20 25

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq AGLLP LLGNAPG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Gln Ile Thr Pro Gly Ser Ala Ala Gly Leu Leu Pro Leu Leu Leu
 -20 -15 -10
 Gly Asn Ala Pro Gly Glu Ser Val Gly Gly Arg Cys Xaa Pro Gly Cys
 -5 1 5 10
 Trp

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5
 seq TWLLLT LQNSVFT/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ile Leu Ser Thr Trp Leu Leu Leu Thr Leu Gln Asn Ser Val Phe
 -15 -10 -5
 Thr Ser Phe Arg Ile Ser Pro Asn Arg Ile Gln Ser Met Leu Pro Pro
 1 5 10 15
 Met

(2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq VCIVLALCHTSRP/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ala Phe His Ser Tyr Trp Gly Lys Ser Leu Gln Ser Phe Lys Thr
-30 -25 -20

Phe Met Arg Val Cys Ile Val Leu Ala Leu Cys His Thr Ser Arg Pro
-15 -10 -5

Met Ser Tyr His Val Pro Leu Ala Ala Gly Ser Pro Leu Met His Trp
1 5 10 15

Ser Pro Cys Ser Pro Val Pro Phe Ile Gly
20 25

(2) INFORMATION FOR SEQ ID NO: 399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq RTLLLLVLHQS/SC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Lys Leu Arg Phe Thr Leu Leu Pro Leu Val Leu His Ser Gln Ser
 -15 -10 -5

Ser Cys Val Phe Trp Lys Ala Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq FIPFLVIYSFVLS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Met Ile Ile Leu Gly Phe Ala Phe Cys Pro Gly His Phe Arg Phe
 -30 -25 -20 -15

Asn Phe Ile Pro Phe Leu Val Ile Tyr Ser Phe Val Leu Ser Ser Pro
 -10 -5 1

His Thr His Arg Glu Pro Tyr Ser Pro Val Ala Asp Phe Asn Glu Cys
 5 10 15

Asn Arg Ser
 20

(2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -27...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq CLLSYIALGAIHA/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

Met Asn Arg Val Pro Ala Asp Ser Pro Asn Met Cys Leu Ile Cys Leu
-25 -20 -15

Leu Ser Tyr Ile Ala Leu Gly Ala Ile His Ala Lys Ile Cys Arg Arg
-10 -5 5

Ala Phe Gln Glu Glu Gly Arg Ala Xaa Ala Lys Thr Gly Val
10 15

(2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -15...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq LFLNLPLVIGTIP/LH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro Leu
-15 -10 -5 1

His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser Met
5 10 15

Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu
20 25

(2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq VIRSTLVLSQCLC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

```
Met Xaa Lys Asn His Arg Asn Lys Lys Ser Ile His Phe Pro Leu Cys
   -70                               -65                               -60

Thr Ile Pro Ser Xaa Met Xaa Lys Ser Cys Thr Leu Pro Leu Gln Arg
   -55                               -50                               -45

Thr Trp Asp Xaa Xaa Pro Ser Phe Val His Trp Xaa Gln Ala Arg Leu
   -40                               -35                               -30

Gln Ser Pro Pro Xaa Ser His Leu Val Xaa Leu Ser Val Ile Arg Ser
  -25                               -20                               -15                               -10

Thr Leu Val Leu Ser Gln Cys Leu Cys Ser Arg Xaa Pro Tyr Phe Ser
           -5                               1                               5

Ala Met Met Thr Pro Lys Cys Lys Ser Ile Xaa Ala Gly Asn Ser Gly
      10                               15                               20

Met Pro Lys Arg Asn Cys Lys Val Leu Pro Ser Ser Glu Lys Met Xaa
    25                               30                               35

Val His
    40
```

(2) INFORMATION FOR SEQ ID NO: 404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1

- (C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq SFIALVYSSLSFQ/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Ser Phe Ile Ala Leu Val Tyr Ser Ser Leu Ser Phe Gln Lys Val
-10 -5 1

Pro Gly

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq IVLFLNSXFPIIC/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

Met Val Phe Asp Thr Leu Lys Ser Arg Ile Val Leu Phe Leu Asn Ser
-20 -15 -10

Xaa Phe Pro Ile Ile Cys Ser Arg
-5 1

(2) INFORMATION FOR SEQ ID NO: 406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -59..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq IFLFSILLMSLRT/FH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

Met Leu Glu Met Glu Met Thr Trp Leu Arg Leu Cys Asp Glu Cys Ser
      -55                      -50                      -45
Arg Trp Gly Met Ala Ser Ala Trp Gly Arg Gly Gly Lys Leu Leu Gly
      -40                      -35                      -30
Ala Gln Val Ala Leu His Pro Arg Asn Cys Ser Lys Ala Lys Ile Phe
      -25                      -20                      -15
Leu Phe Ser Ile Leu Leu Met Ser Leu Arg Thr Phe His Cys Asn Tyr
      -10                      -5                      5
Phe Arg Gly Asn Gly
              10
  
```

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq MLFFLGALCRESG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

```

Met Asp Asp Leu Met Leu Phe Phe Leu Gly Ala Leu Cys Arg Glu Ser
      -15                      -10                      -5
Gly Val Pro Ser Leu Gly Lys Gln Glu Arg Met Arg Ala Tyr Ala Ala
      1                      5                      10                      15
Glu Met Pro Pro Leu Leu Pro Ser Pro Cys Pro Pro Pro Ser His Leu
      20                      25                      30
Pro Lys Pro Ala Ser Pro Cys Pro Tyr Pro Leu Xaa Leu Leu Thr Phe
      35                      40                      45
  
```

Pro Val Gly Val Pro His Leu Pro Gly Thr Arg Leu Gln Cys Gln Gly
 50 55 60
 Leu Gly His Ser Leu Xaa Arg Ala Glu Arg Gly Val Gly Gly Gly Val
 65 70 75
 Ser Pro Gly
 80

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LPTLLLLPVGAPG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Val Leu Gly Ala Leu Asn Leu Pro Ser Gln Glu Leu Pro Thr Leu
 -25 -20 -15 -10
 Leu Leu Leu Pro Val Gly Ala Pro Gly Lys Lys Lys Gly Met Glu Gly
 -5 1 5
 Lys Thr Pro Leu Asp Leu Phe Ala His Phe Gly Pro Glu Pro Gly Asp
 10 15 20
 His Ser Asp Pro Leu Pro Pro Ser Ala Pro Ser Pro Thr Arg Glu Gly
 25 30 35
 Ala Leu Thr Pro Pro Pro Gly
 40 45

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq QTFVSELSIPVLG/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

```

Met Leu Val Ser Lys Ile Gln Thr Phe Val Ser Phe Leu Ser Ile Pro
      -15                      -10                      -5

Val Leu Gly Leu Val Pro Asp His Ile Leu Gln Leu Ile Thr Glu Lys
      1                      5                      10

Glu Thr
      15

```

(2) INFORMATION FOR SEQ ID NO: 410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLSTGILGTQA/FR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

```

Met Cys Asn Pro Val Ala His Thr Phe Arg Gly Val His Glu His His
      -30                      -25                      -20

Ala Met Leu Leu Ser Thr Gly Leu Asn Ile Leu Gly Thr Gln Ala Phe
      -15                      -10                      -5                      1

Arg Tyr Glu Asp Gly Gln Leu
      5

```

(2) INFORMATION FOR SEQ ID NO: 411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq ILLWEACTGRCQA/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys Gln
-15 -10 -5

Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu Val
1 5 10 15

Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp Ala
20 25 30

Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala Gly
35 40 45

Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val Lys
50 55 60

Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: . score 4.6
seq VLCILGCHGNLCC/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Thr Gly Tyr Pro Trp Ala Asn Ser Ile Thr Thr Val Leu Cys Ile
-25 -20 -15 -10
Leu Gly Cys His Gly Asn Leu Cys Cys Glu Pro Ala Val Arg Ala Leu
 -5 1 5
Gly

(2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
 - (D) DEVELOPMENTAL STAGE: Fetal
 - (F) TISSUE TYPE: kidney
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: -24..-1
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 4.6
seq IFTALFLXLHSA/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Val Ser Cys Asp Val Xaa Ser Tyr Val Ile Ile Phe Thr Ala Leu
 -20 -15 -10
Phe Leu Xaa Leu His Ser Val Ala Ile Asn Glu Glu Phe
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: AMINO ACID
 - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PROTEIN
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -20..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.6
 seq LFAIFLMCLKSIG/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Lys Ser Phe Asp Lys Lys Leu Phe Ala Ile Phe Leu Met Cys Leu
 -20 -15 -10 -5

Lys Ser Ile Gly Ser Val Val Met Pro Gln Pro
 1 5

(2) INFORMATION FOR SEQ ID NO: 415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -33..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.5
 seq LASLFGLDQXAXG/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

Met Phe Gly Ala Gly Asp Glu Asp Asp Thr Asp Phe Leu Ser Pro Ser
 -30 -25 -20

Gly Gly Ala Arg Leu Ala Ser Leu Phe Gly Leu Asp Gln Xaa Ala Xaa
 -15 -10 -5

Gly His Gly Asn Glu Phe Phe Gln Tyr Thr Ala Pro Lys Gln Pro Lys
 1 5 10 15

Lys Gly Gln Gly Thr Ala Ala Thr Gly Asn Gln Ala Xaa Pro Lys Thr
 20 25 30

Ala Pro Ala Xaa Met Ser Thr Pro Thr Ile Leu Val Ala Thr Ala Val
 35 40 45

His Ala Tyr Arg Tyr Thr Xaa Gly Xaa Tyr Val Lys Gln Xaa Asn Leu
 50 55 60

Val Leu Gln Phe Trp
65

(2) INFORMATION FOR SEQ ID NO: 416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -28..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RFLSLSAADGXDX/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Val Leu Thr Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg
-25 -20 -15

Phe Leu Ser Leu Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser
-10 -5 1

Trp Asp Val Glu Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile
5 10 15 20

Arg Ala Val Ser His Thr Asp Val Thr Lys Lys Asp Leu Lys
25 30

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq LTSVFQAMIWSQG/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Val Ile Glu Leu Thr Ser Val Phe Gln Ala Met Ile Trp Ser Gln
-15 -10 -5
Gly Val Ser Asp Ser Ser Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -50..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq ILFLFYFPAAYYA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

Met Glu Ser Thr Leu Gly Ala Gly Ile Val Ile Ala Glu Ala Leu Gln
-50 -45 -40 -35
Asn Gln Leu Ala Trp Leu Glu Asn Val Trp Leu Trp Xaa Xaa Leu Xaa
-30 -25 -20
Xaa Xaa Ile Pro Xaa Ile Leu Phe Leu Phe Tyr Phe Pro Ala Ala Tyr
-15 -10 -5
Tyr Ala Ser Arg Arg Val Gly Ile Ala Val Leu Trp Ile Ser Leu Ile
1 5 10
Thr Glu Trp Leu
15

(2) INFORMATION FOR SEQ ID NO: 419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -25..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq VLVGVFLSTFLYC/EC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Ile Ile Val Ser Glu Leu Gly Thr Pro Thr Gly Val Leu Val Gly
-25 -20 -15 -10

Val Phe Leu Ser Thr Phe Leu Tyr Cys Glu Cys Val Lys Gly Pro
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -22..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq GFLLCPLVCGLRR/WT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

Met Asn Trp Asn Val Arg Gly Thr Arg Gly Phe Leu Leu Cys Pro Leu
-20 -15 -10

Val Cys Gly Leu Arg Arg Trp Thr Ser Pro Asp Cys Cys Leu Ile Glu
-5 1 5 10

Lys Thr His Arg Gly
15

Leu Thr Asp Phe Tyr Leu Phe Arg Ser Asp Gly
5 10

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq SLLFIFRSILISC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

Met Ser Leu Leu Phe Ile Phe Arg Ser Ile Leu Ile Ser Cys Phe Ser
 -10 -5 1

Gly Asp Phe Phe Phe Phe
 5

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq SKVLIQLSQAFWA/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

Met Pro Leu Ile Ser Lys Val Leu Ile Gln Leu Ser Gln Ala Phe Trp
 -15 -10 -5

Ala Ser Pro Glu Gly Arg Asn Ser Ser Gly Ser Lys Arg Lys Gln Leu
 1 5 10 15
 Val Ala Ala Val Glu Met Arg Tyr Cys Lys Arg Gln Gln Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
 -25 -20 -15
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
 -10 -5 1
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser Arg Ser Asn Lys
 5 10 15
 Phe Gln Asn Ser Ser Val Glu Asp Asp Asp Val Val Phe Ile Glu
 20 25 30 35
 Pro Val Gln Pro Pro Pro Pro Ser Val Pro Val Val Ala Asp Gln Arg
 40 45 50
 Thr Ile Thr Phe Thr Ser Ser Lys Asn Xaa Glu Leu Gln Gly Asn Asp
 55 60 65
 Ser Lys Ile Thr Pro Ser Ser Lys Glu Leu Ala S.
 70 75

(2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq ILLLTHVPPWILE/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Asp Thr Gly Glu Ser Phe Ser Pro His Thr Ser Cys Arg Gly His
-30 -25 -20
Trp Arg Ile Leu Leu Leu Thr His Val Pro Pro Trp Ile Leu Glu Asn
-15 -10 -5 1
Pro Ser Cys His Thr Arg Pro Ala Val Asp Thr Gly Glu Ser Phe Ser
5 10 15
Pro Gln Arg
20

(2) INFORMATION FOR SEQ ID NO: 427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq LVLLSVLKEPVSR/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

Met Pro Tyr Leu Asp Pro Tyr Ile Thr Gln Pro Ile Ile Gln Ile Glu
-30 -25 -20
Arg Lys Leu Val Leu Leu Ser Val Leu Lys Glu Pro Val Ser Arg Ser
-15 -10 -5 1

Ile Phe Asp Tyr Ala Leu Arg Ser Lys Asp Ile Thr Ser Leu Phe Arg
 5 10 15
 His Leu His Met Arg Gln Lys Lys Arg Asn Gly Ser Leu Pro Asp Cys
 20 25 30
 Pro Pro Pro Glu Asp Pro Ala Ile Ala Gln Leu Leu Lys Lys Leu Leu
 35 40 45
 Ser Gln Gly Met Thr Glu Glu Glu Glu Asp Lys Leu Leu Ala Leu Lys
 50 55 60 65
 Asp Phe Met Met

(2) INFORMATION FOR SEQ ID NO: 428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq VLLGSTAMATSLT/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

Met Asp Thr Ser Ser Val Gly Gly Leu Glu Leu Thr Asp Gln Thr Pro
 -25 -20 -15
 Val Leu Leu Gly Ser Thr Ala Met Ala Thr Ser Leu Thr Asn Val Gly
 -10 -5 1
 Asn Ser Phe Ser Gly Pro Ala Asn Pro Leu Val Ser
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq FGLLDFVQCCDS/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

Met His Val Leu Phe Asn Ile Val Thr Thr Asn Xaa Xaa Asn His Phe
 -25 -20 -15

Gly Leu Leu Asp Phe Val Val Gln Cys Cys Asp Ser Leu Arg Asn His
 -10 -5 1

Xaa Xaa Ser Phe Gln Ser Ser Tyr Leu Arg Leu Asn His Ser Xaa His
 5 10 15 20

Thr Cys

(2) INFORMATION FOR SEQ ID NO: 430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq TAYWLSFMSWAQS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

Met Pro Pro Gln Ser Cys Cys Ser Lys Thr Ala Tyr Trp Leu Ser Phe
 -20 -15 -10

Met Ser Trp Ala Gln Ser Ser Ser Phe Gly Ser Arg Xaa Glu Ser Thr
 -5 1 5 10

Ser Pro Cys Thr Asp His Cys Ser Gly Pro Arg Glu Glu Gln Leu Cys
 15 20 25

Ser Ser Arg Val Phe His Cys Ile Thr His Pro Asn Gly Arg Ile His

30

35

40

Arg Trp

(2) INFORMATION FOR SEQ ID NO: 431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SCVFFHFLQGGLG/FG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Ser Cys Val Phe Phe His Phe Leu Gln Gly Gly Leu Gly Phe Gly
 -10 -5 1

Ser Ala Gly Arg Cys Ala Gly Asp Arg
 5 10

(2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq LILLPIWINMAQI/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met Ser Ile Ser Leu Ser Ser Leu Ile Leu Leu Pro Ile Trp Ile Asn
 -20 -15 -10 -5
 Met Ala Gln Ile Gln Gln Gly Gly Pro Asp Glu Lys Glu Lys Thr Thr
 1 5 10
 Ala Leu Lys Asp Leu Leu Ser Arg Ile Asp Leu Asp Glu Leu Met Lys
 15 20 25
 Lys Asp Glu Pro Pro Gly
 30

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34...-1
- (C) IDENTIFICATION METHOD: Von Helms matrix
- (D) OTHER INFORMATION: score 4.2
seq SFCNAVVLSPVEQ/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

Met Thr Ala Leu Asn Leu Val Ala Pro Phe Ser Asp Gly Asp Ser Gly
 -30 -25 -20
 Ser Val Ser Leu Ala Ser Phe Cys Asn Ala Val Val Leu Ser Pro Val
 -15 -10 -5
 Phe Gln Glu Glu Glu His Leu Leu Phe Gln Lys Arg Lys Thr Lys Thr
 1 5 10
 Trp Pro Pro Arg
 15

(2) INFORMATION FOR SEQ ID NO: 434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.2
seq PVQVLGLLATCQH/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

Met Trp Ser Arg Pro Val Gln Val Leu Gly Leu Leu Ala Thr Cys Gln
-15 -10 -5
His Ala Pro Ser Pro Ser Phe Lys Gly Glu Thr Cys Thr Glu Ile Glu
1 5 10 15
Ser Val Tyr Leu Ala Pro Met
20

(2) INFORMATION FOR SEQ ID NO: 435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -24..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.2
seq SLNQILLFLLISC/RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

Met Arg Tyr Arg Leu Arg Ile Gln Ile Thr Thr Ser Leu Asn Gln Ile
-20 -15 -10
Leu Leu Phe Leu Leu Ile Ser Cys Arg Thr Leu Ser
-5 1

(2) INFORMATION FOR SEQ ID NO: 436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq VLLFFCCSPLYSP/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

```

Met Pro Phe Phe Ser Asn Gln Pro Thr Gln Val Ser Val Leu Leu Phe
-25                -20                -15                -10

Phe Cys Cys Ser Pro Leu Tyr Ser Pro Leu Phe Leu Leu Xaa Leu Ile
          -5                1                5

Pro His Gln
          10

```

(2) INFORMATION FOR SEQ ID NO: 437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq IAVGLTCQHVSHA/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

```

Met Arg Val Lys Asp Pro Thr Lys Ala Leu Pro Glu Lys Ala Lys Arg
          -40                -35                -30

Ser Lys Arg Pro Thr Val Pro His Asp Glu Asp Ser Ser Asp Asp Ile
          -25                -20                -15

Ala Val Gly Leu Thr Cys Gln His Val Ser His Ala Ile Ser Val Asn
          -10                -5                1

```

His Val Lys Arg Ala Ile Ala Glu Asn Leu Trp Ser Val Cys Ser Glu
 5 10 15 20
 Cys Leu Lys Glu Arg Arg Phe Tyr Asp Gly Gln Leu Val Leu Thr Ser
 25 30 35
 Asp Ile Trp Leu Cys Leu Lys Cys Gly Phe Gln Gly Cys Gly Lys Asn
 40 45 50
 Ser Glu Ser Gln His Ser Leu Lys His Phe Lys Ser Ser Arg Thr Glu
 55 60 65
 Pro Leu Arg
 70

(2) INFORMATION FOR SEQ ID NO: 438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq GTYLTFPSPLCQL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

Met Val Ser Leu Gly Tyr Tyr Leu Ile Phe Val Leu Tyr Leu Trp Leu
 -40 -35 -30
 Cys Phe Met Gln Ile Ser Glu Glu Lys Leu Ile Glu Glu His Thr Gly
 -25 -20 -15
 Thr Tyr Leu Thr Ser Ser Ser Pro Leu Cys Gln Leu Gln Pro Pro Gly
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq VLCCLLIATPTFF/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Ser Leu Thr Ser Arg Xaa Xaa Ile Met Xaa Thr Ile Lys Ile Gln
-35 -30 -25 -20
Asn Ile Ser Ile Thr Lys Val Leu Cys Cys Leu Leu Ile Ala Thr Pro
-15 -10 -5
Thr Phe Phe Leu Leu Leu Pro Ser Ser Ile Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq AGVVSTSVAAAVA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Xaa Ala Glu Ala Ala Gly Val Val Ser Thr Ser Val Ala Ala Ala
-15 -10 -5
Val Ala Ala Val Ala Ala Pro Ala Gly Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq IMSSCLALTYTNS/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

Met Trp Ile Met Ser Ser Cys Leu Ala Leu Thr Tyr Thr Asn Ser Ile
-15          -10          -5          1
Ser His Ser Leu Cys Leu Glu Arg Ala Tyr Ser Leu Phe Lys Val Asp
          5          10          15

```

(2) INFORMATION FOR SEQ ID NO: 442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq SNALVLVTRGSSS/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

Met Pro Arg Gly Val Tyr Asn Ser Asn Ala Leu Val Leu Val Thr Arg
-20          -15          -10          -5
Gly Ser Ser Ser Leu Pro Leu Gly Leu Tyr Gly Ile Asn Cys Val Gln
          1          5          10
Val Ile Lys Leu Phe Tyr Arg Gly His Leu His Trp Glu Thr Leu Leu
          15          20          25

```

Pro Ser
30

(2) INFORMATION FOR SEQ ID NO: 443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq FLLPCVHPFSVIA/VY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Ile Glu Pro Cys Glu Lys Met Lys His Tyr Asp Met Asn Trp Phe
 -40 -35 -30

Leu Cys Met Tyr Glu Cys Phe Phe Phe His Leu Leu Glu Thr Glu Phe
 -25 -20 -15

Leu Leu Pro Cys Val His Pro Phe Ser Val Ile Ala Val Tyr Val Phe
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq AALCGISLSQXFP/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq ATLRCWASTPVSG/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

```

Met Arg Lys Ile Ser His Cys Leu His Cys Trp Pro Glu Ser Gly Ala
   -25                               -20                               -15

Thr Leu Arg Cys Trp Ala Ser Thr Pro Val Ser Gly Arg Leu Ser Ser
   -10                               -5                               1

Met Ala Val Xaa Xaa Xaa Gly Glu Xaa Pro Pro Gln Asp Ala Phe Thr
   5                               10                               15                               20

Thr Gln Trp Leu Val Arg Asp Leu Arg Gly Lys Thr Glu Lys Glu Phe
   25                               30                               35

Lys Ala Tyr Val Ser Leu Phe Met Arg His Leu Cys Glu Pro Gly Ala
   40                               45                               50

Asp Gly Ser Glu Thr Phe Ala Asp Gly Val Pro Arg Glu Gly Leu Ser
   55                               60                               65

Arg Gln Gln Val Leu Thr Arg Ile Gly Val Met Ser Leu Val Lys Lys
   70                               75                               80

Lys Gly Gln
   85

```

(2) INFORMATION FOR SEQ ID NO: 447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq LLHPCGSITLTSS/ST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

```

Met Cys Ile Asn Asp His Ile Ile Lys Leu Leu His Pro Cys Gly Ser

```

-20 -15 -10
 Ile Thr Leu Thr Ser Ser Ser Thr Thr Arg
 -5 1

(2) INFORMATION FOR SEQ ID NO: 448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq VALQCGLTIPALX/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

Met Arg Cys Arg Val Ala Leu Gln Cys Gly Leu Thr Ile Pro Ala Leu
 -15 -10 -5
 Xaa Leu Pro Gln Gly Asp Glu Ala Gly Asp Ala Gln Asp Leu Arg Gly
 1 5 10 15
 Pro Ala Gln Ala Glu Tyr Leu Tyr Ile Ile Ser Pro Ser
 20 25

(2) INFORMATION FOR SEQ ID NO: 449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -93..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9

seq LTSAFLWLPRLHI/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

```

Met Thr Val Arg Tyr Gly Lys Phe Leu Ser Leu Leu Lys Asp Gly Ala
      -90      -85      -80
Glu Asn Asp Leu Thr Trp Val Leu Lys His Cys Glu Arg Phe Leu Lys
      -75      -70      -65
Gln Gln Gln Thr Ser Ile Lys Ser Ser Leu Leu Cys Leu Gln Gly Asn
      -60      -55      -50
Tyr Ala Gly His Asp Trp Phe Val Ser Ser Leu Phe Met Ile Met Leu
      -45      -40      -35      -30
Gly Asp Lys Glu Lys Thr Phe Gln Phe Leu His Gln Phe Ser Arg Leu
      -25      -20      -15
Leu Thr Ser Ala Phe Leu Trp Leu Pro Arg Leu His Ile Ser Val Arg
      -10      -5      1
Leu Gln Ser Val Phe Lys Gly Gly Phe Xaa Ile Leu Arg Thr Leu Tyr
      5      10      15
Leu His Ser Xaa Gly Arg
      20      25

```

(2) INFORMATION FOR SEQ ID NO: 450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq FFVVVLFSAAGCKV/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

```

Met Ala Phe Asp Val Ser Cys Phe Phe Trp Val Val Leu Phe Ser Ala
      -20      -15      -10      -5
Gly Cys Lys Val Ile Thr Ser Trp Asp Gln Met Cys Ile Glu Lys Glu
      1      5      10

```

Ala Thr

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq HLSSTSPPWTHA/AI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

Met Leu Thr Arg Leu Val Leu Ser Ala His Leu Ser Ser Thr Thr Ser
-20 -15 -10

Pro Pro Trp Thr His Ala Ala Ile Ser Trp Glu Leu Asp Asn Val Leu
-5 1 5 10

Met Pro Ser Pro Arg Ile Trp Pro Leu
15

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq CVNLLLGFEPPVIS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

```

Met Arg Tyr Phe Gln Gly Pro Ser Pro Tyr Ser Glu Ile Glu Ile Glu
-40          -35          -30          -25

Leu Cys Asp His Val Tyr Ser Phe Gln Gly Leu Cys Val Asn Leu Leu
          -20          -15          -10

Leu Gly Phe Glu Pro Val Ile Ser Arg Ser Arg Xaa Ser Ser Leu Ala
          -5          1          5

Val Glu Ser
10

```

(2) INFORMATION FOR SEQ ID NO: 453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq LASLECYVPSTNQ/WQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

```

Met Xaa Xaa Lys Arg Thr His Xaa Xaa Xaa Ser Val Phe Asn Gly Leu
-40          -35          -30

Val Tyr Ala Ala Gly Gly Arg Asn Ala Glu Gly Ser Leu Ala Ser Leu
-25          -20          -15          -10

Glu Cys Tyr Val Pro Ser Thr Asn Gln Trp Gln Pro Lys Xaa Xaa Leu
          -5          1          5

Glu Val Ala Arg Cys Cys His Ala Ser Ala Val Ala Asp Gly Arg Val
10          15          20

Leu Val Thr Gly Gly Leu
25

```

(2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -38..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LLFFHLLLNDFFT/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

```

Met Phe Leu Lys Val Gln Ser Gln Ser Phe Tyr Xaa Pro Tyr Arg Asp
   -35                      -30                      -25

Cys Leu Asn Phe His Lys Ser Thr Tyr Leu Leu Phe Phe His Leu Leu
   -20                      -15                      -10

Leu Asn Asp Phe Phe Thr Phe Tyr Xaa Ala Lys
   -5                      1                      5

```

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq WIILIIYTFQCNS/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

```

Met Gln Pro Leu Lys Ile Ile Phe Tyr Leu Ser Val Ser Ile Trp Ile
   -25                      -20                      -15

Ile Leu Ile Ile Tyr Thr Phe Gln Cys Asn Ser Ser Leu Ser Ile Leu
   -10                      -5                      5

Leu Leu Glu Leu

```

(2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq RVAACTAAAPLQA/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala Ala Pro
 -15 -10 -5

Leu Gln Ala His Gly Ala Xaa Ile Gln Gln Xaa Pro Asp Xaa Leu Xaa
 1 5 10

Ser Xaa Arg Leu Ser Arg Xaa Gly Leu Ser Ala Gly Arg Leu His Gln
 15 20 25

Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly Arg Ala
 30 35 40

(2) INFORMATION FOR SEQ ID NO: 457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq RWASSCLHPSARS/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

```

Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro Arg Pro Ala Leu Pro
      -30                -25                -20

Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys Leu His Pro Ser Ala
      -15                -10                -5

Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg Thr Pro
      1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LCPVIFPPSNCWK/EY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

```

Met Gln Gly Val Arg Gly Pro Val Ser Phe Ser Trp Ser Thr Thr Met
      -25                -20                -15

Leu Cys Pro Val Ile Phe Phe Pro Ser Asn Cys Trp Lys Glu Tyr Asn
      -10                -5                1

Arg Thr Gln
      5

```

(2) INFORMATION FOR SEQ ID NO: 459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq FXLLFXFXFFRQ/XG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Xaa Xaa Phe Ser Phe Xaa Leu Leu Phe Xaa Xaa Phe Xaa Phe Phe
-15 -10 -5

Arg Gln Xaa Gly
1

(2) INFORMATION FOR SEQ ID NO: 460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq SVRLFRFSVIMA/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Leu Leu Leu Ser Glu Ala Leu Ser Glu Ser Val Arg Leu Leu Phe
-20 -15 -10

Arg Phe Ser Val Ile Met Ala Ser Glu Lys Gln Ser Phe Gln Ile
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -17..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.8
seq SLPCTTAEPPLLSS/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

Met Ala Leu Ile Ser Leu Pro Cys Thr Thr Ala Phe Pro Leu Leu Ser
-15 -10 -5

Ser Lys Val Ser Gln Leu Leu Leu Pro Leu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO: 462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -37..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.8
seq RVVALPLVRATCT/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ser Glu Glu Glu Ala Ala Gln Ile Pro Arg Ser Ser Val Trp Glu
-35 -30 -25

Gln Asp Gln Gln Asn Val Val Gln Arg Val Val Ala Leu Pro Leu Val
-20 -15 -10

Arg Ala Thr Cys Thr Ala Val Cys Asp Val Tyr Ser Ala Ala Lys Asp
-5 1 5 10

Arg His Pro Leu Leu Gly Ser Ala Trp
15 20

(2) INFORMATION FOR SEQ ID NO: 463:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LAELTVDPQGALA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```

Met Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly Pro
  -70                      -65                      -60

Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly Ile
  -55                      -50                      -45

Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile Lys
  -40                      -35                      -30                      -25

Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu Thr
          -20                      -15                      -10

Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val Ile
          -5                      1                      5

Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys Phe
  10                      15                      20

Arg
  25

```

(2) INFORMATION FOR SEQ ID NO: 464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -117..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.8
seq XXXYLNECPVCYC/FS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

```

Met Asn Ser Gly Gly Gly Phe Gly Leu Gly Leu Gly Phe Gly Leu Thr
-115                      -110                      -105

Pro Thr Ser Val Ile Gln Val Thr Asn Leu Ser Ser Ala Val Thr Ser
-100                      -95                      -90

Glu Gln Met Arg Thr Leu Phe Ser Phe Leu Gly Glu Ile Glu Glu Leu
-85                      -80                      -75                      -70

Arg Leu Tyr Pro Pro Asp Asn Ala Pro Leu Ala Phe Ser Ser Xaa Val
-65                      -60                      -55

Cys Tyr Val Lys Phe Arg Asp Pro Ser Ser Val Gly Val Ala Gln His
-50                      -45                      -40

Leu Thr Asn Thr Val Phe Ile Asp Arg Xaa Leu Xaa Ser Cys Ser Leu
-35                      -30                      -25

Cys Arg Arg Leu Val Ser Arg Phe Xaa Xaa Xaa Tyr Leu Asn Phe Cys
-20                      -15                      -10

Pro Val Cys Tyr Cys Phe Ser Phe Pro Arg Asp Trp Gln Val Asp Ser
-5                      1                      5                      10

Thr Leu

```

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -13...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.7
seq MIEMLIFLDCVLS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

```

Met Ile Glu Met Leu Ile Phe Leu Asp Cys Val Leu Ser Ser Lys Asp
-10                      -5                      1

```

Thr Ile Thr Met Phe Val Lys Phe Ile Pro Ile Phe Pro Phe Pro Leu
 5 10 15
 Gln Phe Tyr Leu Pro Ser Phe Leu Leu Leu Glu
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq VIGSLLVLTMLTC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met His Pro Phe Leu Ala Ala His Gly Pro Ala Phe His Lys Gly Tyr
 -75 -70 -65
 Lys His Ser Thr Ile Asn Ile Val Asp Ile Tyr Pro Met Met Cys His
 -60 -55 -50
 Ile Leu Gly Leu Lys Pro His Pro Asn Asn Gly Thr Phe Gly His Thr
 -45 -40 -35
 Lys Cys Leu Leu Val Asp Gln Trp Cys Ile Asn Leu Pro Glu Ala Ile
 -30 -25 -20
 Ala Ile Val Ile Gly Ser Leu Leu Val Leu Thr Met Leu Thr Cys Arg
 -15 -10 -5 1

Arg

(2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -14..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IWPMASVATLWS/FT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Ile Trp Pro Met Ser Ala Ser Val Ala Thr Leu Trp Ser Phe Thr
 -10 -5 1
Ser Tyr Ile Ser Tyr Pro Ser Arg Phe Tyr Tyr Asp Ala Trp
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -31..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq LFIYLVFECLLC/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp Phe His Pro
-30 -25 -20
Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu Leu Cys Thr
-15 -10 -5 1
Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn Ala Gln Ile
 5 10 15
Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys Pro Phe Lys
 20 25 30
Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu Arg Ile Glu
 35 40 45
Cys Gln Gly Asn Gly

50

(2) INFORMATION FOR SEQ ID NO: 469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -87..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq LILQASLKGELEA/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```

Met Lys Glu Leu Asn Gln Lys Leu Thr Asn Lys Asn Asn Lys Ile Glu
-85                               -80                               -75

Asp Leu Glu Gln Glu Ile Lys Ile Gln Lys Gln Lys Gln Glu Thr Leu
-70                               -65                               -60

Gln Glu Glu Ile Thr Ser Leu Gln Ser Ser Val Gln Glu Tyr Glu Glu
-55                               -50                               -45                               -40

Lys Asn Xaa Lys Ile Lys Gln Leu Leu Val Lys Thr Lys Lys Glu Leu
-35                               -30                               -25

Ala Asp Ser Lys Gln Ala Glu Thr Asp His Leu Ile Leu Gln Ala Ser
-20                               -15                               -10

Leu Lys Gly Glu Leu Glu Ala Ser Gln Gln Gln Val Glu Val Tyr Lys
-5                               1                               5

Val Arg Val Leu Leu Phe Lys Ile Lys Lys Met Phe Phe His Val Glu
10                               15                               20                               25

Val Arg Asn Gly

```

(2) INFORMATION FOR SEQ ID NO: 470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -113..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq RLLLCILIIVCYI/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

```

Met Gly Asn Thr Leu Lys Glu Met Gln Asp Val Gln Gly Ala Leu Gln
      -110                      -105                      -100

Cys Tyr Thr Arg Ala Ile Gln Ile Asn Pro Ala Phe Ala Asp Ala His
      -95                      -90                      -85

Ser Asn Leu Ala Ser Ile His Lys Asp Ser Gly Asn Ile Pro Glu Ala
      -80                      -75                      -70

Ile Ala Ser Tyr Arg Thr Ala Leu Lys Leu Lys Pro Asp Phe Pro Asp
      -65                      -60                      -55                      -50

Ala Tyr Cys Asn Leu Ala His Cys Leu Gln Ile Val Cys Asp Trp Thr
      -45                      -40                      -35

Asp Tyr Asp Glu Arg Met Lys Lys Leu Val Ser Ile Val Ala Asp Gln
      -30                      -25                      -20

Leu Glu Lys Asn Arg Leu Leu Leu Cys Ile Leu Ile Ile Val Cys Tyr
      -15                      -10                      -5

Ile Leu Phe Leu Met
      1

```

(2) INFORMATION FOR SEQ ID NO: 471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (C) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq VAYAIPSPISLFC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

Met Leu Ile Leu Ala Asp Thr Arg Arg Val Gln Gly Gly Thr Leu Gly
 -35 -30 -25

Leu Ile Pro Ala Val Leu Asn Arg Val His Val Ala Tyr Ala Ile Pro
 -20 -15 -10

Ser Ile Pro Ser Leu Phe Cys Gln Arg Trp
 -5 1

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq CVFLFPLISNTSS/YK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

Met Leu Val Gly Ile Tyr Phe Cys Val Phe Leu Phe Pro Leu Ile Ser
 -20 -15 -10 -5

Asn Thr Ser Ser Tyr Lys Asn Cys His Lys Thr Leu Gln His Thr Ile
 1 5 10

Pro Pro His Gly
 15

(2) INFORMATION FOR SEQ ID NO: 473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -42..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq LLLQGACPLIFL/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

Met Phe Leu Ala Pro Ser Leu Leu Ile Thr Lys Leu Leu Thr Gly Ser
-40 -35 -30
Glu Ser Pro Asp Gly Asn Pro Pro Ala Leu Gly Arg Pro Leu Leu Leu
-25 -20 -15
Gln Gly Ala Cys Pro Cys Leu Ile Phe Leu Arg Pro Asp Glu Asn Lys
-10 -5 1 5
Lys Glu Gly Xaa Glu Glu Lys Lys Asn His Lys Leu Pro Leu Lys Thr
10 15 20
Ser Leu Gly
25

(2) INFORMATION FOR SEQ ID NO: 474:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -18..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq SKSCLFYLQKVSG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

Met Asp Pro Ser Ala Ser Lys Ser Cys Leu Phe Tyr Leu Gln Lys Val
-15 -10 -5
Ser Gly Ile Pro Gly Leu Leu Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq RWLCLQAYLASFS/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Ser Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val
-45 -40 -35

Gly Gly Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser
-30 -25 -20 -15

Gln Arg Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu
-10 -5 1

Ser Pro His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro
5 10 15

Pro Pro
20

(2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq AQLASFLLPGATP/VA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Lys Tyr Gln Met Val Ser Gly Ser Ala Gln Leu Ala Ser Pro Leu
-20 -15 -10
Leu Pro Gly Ala Thr Pro Val Ala Gly Thr Ile Leu Lys Ser Leu Leu
-5 1 5 10
Leu Arg Thr Val Lys Met Met Arg Val Met
15 20

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq CFWGLMYXWLLLG/SX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

Met Asn Gly Thr Phe Pro Gly Thr Tyr Val Tyr Leu Val Ala Tyr Gly
-35 -30 -25 -20
Asp Leu Arg Ile Phe Gly Cys Phe Trp Gly Leu Met Tyr Xaa Trp Leu
-15 -10 -5
Leu Leu Gly Ser Xaa Gly
1

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 12.7
seq ILFLLSWSGPLQG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

```

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp Ser
-20..                -15                -10

Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met Glu Arg
-5                1                5                10

Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln Asp Gln Ser
15                20                25

Ser Arg His Ala Ala Glu Leu Arg Asn Phe Lys Asn Lys Met Leu Pro
30                35                40

Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala Leu Arg Thr Glu Ala
45                50                55

Xaa Thr Ile Ser Xaa Gly Val Asp Arg Leu Glu Arg Glu Val Asp Tyr
60                65                70                75

Leu

```

(2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -22..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LMLLVSSLSPVQG/VL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

```

Met Lys Phe Ile Ser Thr Ser Leu Leu Leu Met Leu Leu Val Ser Ser
-20                -15                -10

```

Leu Ser Pro Val Gln Gly Val Leu Glu Val Tyr Tyr Thr Ser Leu Arg
 -5 1 5 10
 Cys Arg Cys Val Gln Glu Ser Ser Val Phe Ile Pro Arg Arg Phe Ile
 15 20 25
 Asp Arg Ile Gln Ile Leu Pro Arg Gly Asn Gly Cys Pro Arg Lys Glu
 30 35 40
 Ile Ile Val Trp Lys Lys Asn Lys Ser Ile Val Cys Val Asp Leu Lys
 45 50 55
 His Arg
 60

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq VLELLAAVCLVRG/GH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

Met Asn Tyr Gln Tyr Gly Phe Asn Met Val Met Ser His Pro His Ala
 -45 -40 -35
 Val Asn Glu Ile Ala Leu Ser Leu Asn Asn Lys Asn Pro Arg Thr Lys
 -30 -25 -20
 Ala Leu Val Leu Glu Leu Leu Ala Ala Val Cys Leu Val Arg Gly Gly
 -15 -10 -5 1
 His Glu Ile Ile Leu Ser Ala Phe Asp Asn Phe Lys Glu Val Cys Gly
 5 10 15
 Glu Lys Gln Arg Phe Glu Lys Leu Met Glu His Phe Arg Asn Glu Asp
 20 25 30
 Asn Asn Ile Asp Phe Met Val Ala Ser Met Gln Phe Ile Asn Ile Val
 35 40 45
 Val His Ser Val Glu Asp Met Asn Phe Arg Val His Leu Gln Tyr Glu
 50 55 60 65

Phe Thr Lys Leu Gly Leu Xaa Glu Tyr Leu Xaa Lys Leu Lys His Thr
 70 75 80

Glu Ser Asp Lys Leu Gln Val Gln Ile
 85 90

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.7
 seq LVMCFLSYFGTFA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

Met Ala Gln Ser Ile His Met Tyr Ala Ala Arg Val Gln Trp Gly Leu
 -25 -20 -15

Val Met Cys Phe Leu Ser Tyr Phe Gly Thr Phe Ala Val Glu Phe Arg
 -10 -5

His Tyr Arg Tyr Glu Ile Val Cys Ser Glu Tyr Gln Glu Asn Phe Leu
 5 10 15 20

Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser Glu Tyr Gln
 25 30

(2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.1
 seq LHLFHLIRPXQG/WX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Gly Ser Gly Tyr Ser His Ser Leu His Leu Phe His Leu Leu Ile
 -20 -15 -10
 Arg Pro Xaa Gln Gly Trp Xaa Xaa Ile Val Pro Ala Cys Phe Trp Arg
 -5 1 5 10
 Lys Lys Ile Leu Thr Pro Ser Thr Gly Thr Met Glu Leu Leu Gln Val
 15 20 25
 Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser Ser Asn Ser Thr Gly
 30 35 40
 Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr Thr Thr Lys Pro
 45 50 55
 Ser Ile Thr Thr Pro Asn Thr Trp
 60 65

(2) INFORMATION FOR SEQ ID NO: 483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: -16..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq CFSLVLLTTSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
 -15 -10 -5
 Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
 1 5 10 15
 Gln Val Ser Cys Arg Ile Met Xaa Xaa Thr Leu Val Ser Lys Lys Ala
 20 25 30

Asn Gln Gln Leu Asn Phe Thr Glu Xaa Xaa Gly Gly Xaa Xaa Ala Ala
 35 40 45
 Gly Thr Lys Phe Gly
 50

(2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq MTCLSVLFGYATS/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu
 -30 -25 -20
 Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr
 -15 -10 -5
 Ser His Pro Gln Gly Leu Tyr Ile
 1 5

(2) INFORMATION FOR SEQ ID NO: 485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3
seq RQLLLPLPPFSFP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

```

Met Pro Gln Gln Pro Val Glu Gln Gly Ser Pro Leu Leu Arg Gln Leu
-25                      -20                      -15

Leu Leu Pro Leu Pro Pro Phe Ser Phe Pro Ala Pro Ser Pro Cys Pro
-10                      -5                      1                      5

Ser Trp Pro Val Ala Leu Gly Ser His Gly Val Ala Tyr Trp Gly Ser
10                      15                      20

Cys Ser Leu Gly His
25

```

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -80..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq RASLLPMLLGSWA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

```

Met Pro Ser Arg Ser Pro Phe Thr Trp Ser His Leu Cys Trp Arg Ala
-80                      -75                      -70                      -65

Gly Arg Cys Pro Arg Trp Arg Ala Cys Leu Ser Ser Ser Ser Val Arg
-60                      -55                      -50

Met Cys Ser Pro Ala Ala Pro Ser Arg Phe Gly Ala Leu Gly Xaa Ser
-45                      -40                      -35

Ala Arg Arg Trp Pro Arg Arg Asp Ala Asp Thr Trp Cys Ala Pro Gln
-30                      -25                      -20

Gly Val Met Arg Ala Ser Leu Leu Pro Met Leu Leu Gly Ser Trp Ala
-15                      -10                      -5

Phe Leu Pro Pro Ser Cys Ser Pro Arg Ala
1                      5                      10

```


(2) INFORMATION FOR SEQ ID NO: 487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6
seq LTYGIILTHGASG/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

Met Ser His Thr Glu Val Lys Leu Lys Ile Pro Phe Gly Asn Lys Leu
-40                      -35                      -30                      -25

Leu Asp Ala Val Cys Leu Val Pro Asn Lys Ser Leu Thr Tyr Gly Ile
                      -20                      -15                      -10

Ile Leu Thr His Gly Ala Ser Gly Asp Met Asn Leu Pro His Leu Met
                      -5                      1                      5

Ser Leu Ala Ser His Leu Ala Ser His Gly Phe Phe Cys Leu Arg Phe
10                      15                      20

Thr Cys Lys Gly Leu Asn Ile Val His Arg Ile Lys Ala Tyr Lys Ser
25                      30                      35                      40

Val Leu Asn Tyr Leu Lys Thr Ser Gly Xaa Tyr Lys Leu Ala Gly
                      45                      50                      55

```

(2) INFORMATION FOR SEQ ID NO: 488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -40..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6
 seq LCXEFKSVASCDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

Met Glu Leu Gly Ser Cys Leu Glu Gly Gly Arg Glu Ala Ala Glu Glu
-40                               -35                -30                -25

Glu Gly Glu Pro Glu Val Lys Lys Arg Arg Leu Leu Cys Xaa Glu Phe
                               -20                -15                -10

Xaa Ser Val Ala Ser Cys Asp Ala Ala Val Ala Gln Cys Phe Leu Ala
                               -5                  1                  5

Xaa Asn Asp Trp Glu Met Glu Arg Ala Leu Asn Ser Tyr Phe Glu Pro
    10                  15                  20

Pro Val Glu Glu Ser Ala Leu Glu Arg Arg Pro Xaa
    25                  30                  35
  
```

(2) INFORMATION FOR SEQ ID NO: 489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -36..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.8
 seq AFVSGLLIGQCSS/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```

Met Gly Arg Thr Tyr Ile Val Glu Glu Thr Val Gly Gln Tyr Leu Ser
-35                               -30                -25

Asn Ile Asn Leu Gln Gly Lys Ala Phe Val Ser Gly Leu Leu Ile Gly
-20                               -15                -10                -5

Gln Cys Ser Ser Gln Lys Asp Tyr Val Ile Leu Ala Thr Arg Thr Pro
    1                  5                  10

Pro Lys Glu Glu Gln Ser Glu Asn Leu
    15                  20
  
```

(2) INFORMATION FOR SEQ ID NO: 490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20                      -15                      -10

Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5                      1                      5                      10

Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15                      20                      25

Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30                      35                      40

Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45                      50                      55

Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60                      65                      70                      75

Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80                      85                      90

Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg
95                      100

```

(2) INFORMATION FOR SEQ ID NO: 491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq CLSCLLIPLALWS/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

```

Met Gly Ser Arg Lys Cys Gly Gly Cys Leu Ser Cys Leu Leu Ile Pro
-20                      -15                      -10
Leu Ala Leu Trp Ser Ile Ile Val Asn Ile Leu Leu Tyr Phe Pro Asn
-5                      1                      5                      10
Gly Gln Thr Ser Tyr Ala Ser Ser Asn Lys Leu Thr Asn Tyr Val Trp
15                      20                      25
Tyr Phe Glu Gly Ile Cys Phe Ser Gly Ile Met Met Leu Ile Val Thr
30                      35                      40
Thr Val Leu Leu Val Leu Glu Asn Asn Asn Asn Tyr Lys Cys Cys Gln
45                      50                      55
Ser Glu Asn Cys Ser Lys Lys Tyr Val Thr Leu Leu Ser Ile Ile Phe
60                      65                      70                      75
Ser Ser Leu Gly Ile Ala Phe Ser Gly Tyr Cys Leu Val Ile Ser Ala
80                      85                      90
Leu Gly Leu Val Gln Gly Pro Tyr Cys Arg Thr Leu Asp Gly Trp Glu
95                      100                      105
Tyr Ala Phe Glu Gly Thr Xaa Gly Arg Phe Leu Thr Asp Ser Ser Ile
110                      115                      120
Trp Ile Gln Cys Leu Glu
125

```

(2) INFORMATION FOR SEQ ID NO: 492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq SFLPSALVIWTS/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

```

Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
-20                               -15                -10

Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr
-5                               1                 5                10

Leu His His Ile
                        15

```

(2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq PLIFSLWCSGVLL/HI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

```

Met Phe Asn Ala Ser Thr Phe Thr Asp Trp Ser Ser Ser Ile Phe Phe
-40                               -35                -30

Val Phe Thr Phe Lys Ser Lys Lys Ser Ala Gly Leu Pro Leu Ile Phe
-25                               -20                -15                -10

Ser Leu Trp Cys Ser Gly Val Leu Leu His Ile His Gln Lys Ala Gly
                        -5                 1                 5

Gly Pro Arg Leu Trp Arg Ile His Gly Glu Gln
                        10                15

```

(2) INFORMATION FOR SEQ ID NO: 494:

Met His Ile Leu Gln Leu Leu Thr Thr Val Asp Asp Gly Ile Gln Ala
-40 -35 -30

Ile Val His Cys Pro Asp Thr Gly Lys Asp Ile Trp Asn Leu Leu Phe
 -25 -20 -15
 Asp Leu Val Cys His Glu Phe Cys Gln Ser Asp Asp Pro Ala Arg
 -10 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq PMQLLQVLSDVLA/EI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

Met Ser Asp Gln Ile Lys Phe Ile Met Asp Ser Leu Asn Lys Glu Pro
 -40 -35 -30
 Phe Arg Lys Asn Tyr Asn Leu Ile Thr Phe Xaa Ser Leu Glu Pro Met
 -25 -20 -15
 Gln Leu Leu Gln Val Leu Ser Asp Val Leu Ala Glu Ile Asp Pro Lys
 -10 -5 1 5
 Gln Leu Val Asp Ile Arg Glu Glu Met Pro Glu Gln Thr Ala Lys Arg
 10 15 20
 Met Leu Ser Leu Leu Gly Ile Leu Lys Tyr Lys Pro Ser Gly Asn Ala
 25 30 35
 Thr Asp Met Ser Thr Phe Arg Gln Gly Leu Val Ile Gly Ser Lys Pro
 40 45 50
 Val Ile Tyr Pro Val Leu
 55

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -79..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq IIHAXGLVRECLA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

Met Ala Thr Ser Ser Gln Xaa Arg Gln Leu Leu Ser Asp Tyr Gly Pro
 -75 -70 -65

Pro Ser Leu Gly Tyr Thr Gln Gly Thr Gly Asn Ser Gln Xaa Pro Gln
 -60 -55 -50

Ser Lys Tyr Ala Glu Leu Leu Ala Ile Ile Xaa Glu Leu Gly Lys Glu
 -45 -40 -35

Ile Arg Pro Met Tyr Ala Gly Ser Lys Ser Ala Met Glu Arg Leu Lys
 -30 -25 -20

Arg Gly Ile Ile His Ala Xaa Gly Leu Val Arg Glu Cys Leu Ala Xaa
 -15 -10 -5 1

Thr Glu Arg Met Pro Asp Pro Ser Cys Leu Val Gly Phe
 5 10

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq LLGAAAVVAALGRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

Met Arg Leu Leu Gly Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
 -15 -10 -5 1
 Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
 5 10 15
 Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
 20 25 30
 Ile Gly Ile Ser Ala His Ile Asp Ser Gly Lys
 35 40

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq RLLLRREFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

Met Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser
 -15 -10 -5
 Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu
 1 5 10 15
 Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro
 20 25 30
 Ala Pro Gly
 35

(2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LNSLSALAEAVG/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

```

Met Phe Arg Leu Asn Ser Leu Ser Ala Leu Ala Glu Leu Ala Val Gly
-15                               -10                               -5

Ser Arg Trp Tyr His Gly Gly Ser Gln Pro Ile Gln Ile Arg Leu Ala
 1              5              10              15

```

(2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -61..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq YTAHSVLAGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

```

Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys Ala Arg
-60                               -55                               -50

Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val Pro Asn
-45                               -40                               -35                               -30

Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro Val Glu
-25                               -20                               -15

Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp Pro Gln
-10                               -5                               1

Ile Ser Glu Ser Asn Phe Ser Pro Lys Phe Asn Glu Lys Asp Gly His
 5              10              15

```

Val Glu Arg Lys Ser Lys Asn Gly Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq TLMFSLTAQWXTS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Met Arg Thr Thr Leu Met Phe Ser Leu Thr Ala Gln Trp Xaa Thr Ser
-15 -10 -5

Arg Ser Ser Phe Gln
1 5

(2) INFORMATION FOR SEQ ID NO: 503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 14.1
seq LTLTLLLTLLAFA/GY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

Met Ser Asp Leu Leu Leu Gly Leu Ile Gly Gly Leu Thr Leu Leu
 -25 -20 -15 -10

Leu Leu Leu Thr Leu Leu Ala Phe Ala Gly Tyr Ser Gly Leu Leu Ala
 -5 1 5

Gly Val Glu Val Ser Ala Gly Ser Pro Pro Ile Arg Asn Val Thr Val
 10 15 20

Ala Tyr Lys Phe His Met Gly Leu Tyr Gly Glu Thr Gly Arg Leu Phe
 25 30 35

Thr Glu Ser Cys Ser Ile Ser Pro Lys Leu Arg Ser Ile Ala Val Tyr
 40 45 50 55

Tyr Asp Asn Pro His Met Val Pro Pro Asp Lys Cys Arg Cys Ala Val
 60 65 70

Gly Ser Ile Leu Ser Glu Gly Glu
 75

(2) INFORMATION FOR SEQ ID NO: 504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4
seq LWSLALWLPLALS/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Gly Thr Glu Met Gly Ala Arg Pro Gly Gly His Pro Xaa Lys
 -30 -25 -20

Trp Ser Phe Leu Trp Ser Leu Ala Leu Trp Leu Pro Leu Ala Leu Ser
 -15 -10 -5

Val Ser Leu Phe Leu Gly Leu Ser Leu Ser Pro Pro Gln Pro Gly Leu
 1 5 10 15

Ser Leu Trp Cys Thr Leu Ser Tyr Cys Cys Glu Gln Trp Lys Phe Lys
 20 25 30

Gly Thr Pro Ser Pro Ala Leu Leu Asn Leu Gly T Arg Gly
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -55..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq LLFALGSLGLIFA/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

```

Met Xaa Phe Leu Arg Lys Val Xaa Ser Ile Leu Ser Leu Gln Val Leu
-55                -50                -45                -40

Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg
-35                -30                -25

Thr Phe Val Xaa Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly
-20                -15                -10

Ser Leu Gly Leu Ile Phe Ala Leu Ile Leu Asn Xaa His Lys Tyr Pro
-5                1                5

Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Xaa Ala Leu Thr
10                15                20                25

Val Ala Val Val Val Thr
30

```

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -38..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 10.1
 seq MLLLLLLGSGQG/PQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg Arg
 -35 -30 -25
 Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu Leu
 -20 -15 -10
 Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -41..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.9
 seq ILPFLLFPFPVNA/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val Thr Ser Asn Thr
 -40 -35 -30
 Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln Ile Leu Pro Phe
 -25 -20 -15 -10
 Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His Xaa Val Ala Gln
 -5 1 5
 Thr Lys Ser Pro Arg
 10

(2) INFORMATION FOR SEQ ID NO: 508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -21...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.7
seq QLCLLLPSCSLVS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

Met Ala Pro Gly Val Ile Ile Ile Gln Leu Cys Leu Leu Leu Pro
-20 -15 -10
Ser Cys Ser Leu Ser Val Ser Gly Cys Ser Cys Pro Ser Ala Cys Phe
-5 1 5 10
Ser Thr Thr Ser Arg Glu
15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: -93...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.6
seq LSLSLGASAPVQC/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509: .

Met Arg His Gly Phe Ile Gln Gln Gln Phe Ser Leu Thr Ala Phe Ser
-90 -85 -80
Xaa Xaa Xaa Xaa Ile Phe Thr Leu Xaa Xaa Leu Ser Gln Leu Leu Ser
-75 -70 -65
Ser Ala Ala Pro Lys His Thr Ala Ala Pro Thr Ala Leu Pro Cys Leu

-60 -55 -50
 Gln Gly Gln Gln Leu Asn Ser Leu Ser Leu Gly Thr Ser Glu Leu Ser
 -45 -40 -35 -30
 Cys Val Leu Ala Ser Ser Cys Leu Ser Thr Lys Thr Asp Pro Ser Gly
 -25 -20 -15
 Leu Ser Leu Ser Leu Gly Ala Ser Ala Pro Val Gln Cys Gln Gln Asp
 -10 -5 1
 Asn Tyr Thr Phe Cys Xaa Gln Tyr Trp Leu Arg Ala Arg His
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LIIFLSFLPFINS/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val Pro Phe Val Arg Gly
 -40 -35 -30
 Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val Ile Leu Ile Ile Phe
 -25 -20 -15 -10
 Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe Val Tyr Lys Thr Asn
 -5 1 5
 Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe Ser Phe Arg Tyr Pro
 10 15 20
 Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu Val Phe
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq FPVLALFLSGSLA/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

Met Ser Leu Ser Gln Arg Gly Phe Pro Val Leu Ala Leu Phe Leu Ser
-20 -15 -10 -5

Gly Ser Leu Ala Leu Phe His His Thr Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
-25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
-10 -5 1

Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
5 10 15

Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
 20 25 30 35
 Val Lys Xaa Pro Pro Arg
 40

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
 -30 -25 -20
 Gly Tyr Gly Val Pro Met Leu Leu Ile Val Gly Gly Ser Phe Gly
 -15 -10 -5
 Leu Arg Glu Phe Ser Xaa Ile Arg Tyr Asp Ala Val Lys Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

(2) INFORMATION FOR SEQ ID NO: 515:

(A) LENGTH: 92 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(A) NAME/KEY: sig_peptide
(B) LOCATION: -90..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.4
seq SLVLLTVTPSRQ/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

Met Ala Gln Ser Gln Gly Trp Val Xaa Arg Tyr Xaa Lys Ala Phe Cys
-90 -85 -80 -75

Lys Gly Phe Phe Val Ala Val Pro Val Ala Val Thr Phe Leu Asp Arg
-70 -65 -50

Val Ala Cys Val Ala Arg Val Glu Gly Ala Ser Met Gln Pro Ser Leu
-55 -50 -45

Asn Pro Gly Gly Ser Xaa Ser Ser Asp Val Val Xaa Xaa Asn His Trp
 -40 -35 -30
 ... Lys Val Arg Asn Phe Glu Val His Arg Gly Asp Ile Val Ser Leu Val
 -25 -20 -15
 Leu Leu Thr Val Thr Pro Ser Xaa Arg Gln Gln Glu
 -10 -5 1

(2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.1
seq WLLVLSFVFGCNV/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

Met Ser Ser Ala Ala Ala Asp His Trp Ala Trp Leu Leu Val Leu Ser
 -20 -15 -10
 Phe Val Phe Gly Cys Asn Val Leu Arg Ile Leu Xaa Pro Xaa Xaa Xaa
 -5 1 5
 Ile Xaa Xaa Val Gln Gly Ala Ala Glu Gly Arg Gly Xaa Glu Ser Gln
 10 15 20 25
 Met Arg Ala Glu Ile Gln Asp Met Lys Gln Glu Leu Ser Thr Val Asn
 30 35 40
 Met Met Asp Glu Phe Ala Arg Tyr Ala Arg Leu Xaa Arg Lys Ile Asn
 45 50 55
 Lys Met Thr Asp Lys
 60

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq HVFFLLLLAHIIA/LE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

Met Asn Leu Phe Lys Thr Asn His Val Phe Phe Leu Leu Leu Leu Ala
-20 -15 -10 -5

His Ile Ile Ala Leu Glu Ser Ile Ala Trp Phe Thr Val Phe Tyr Phe
1 5 10

Gly Asn

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
-20 -15 -10

Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
-5 1 5

Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly
10 15

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -66..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9
seq LLLPRVLTMSG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

```

Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly Gly Pro Ser
-65                               -60                               -55

Ser Thr Val Thr Trp Cys Ala Leu Phe Ser Asn His Val Ala Ala Thr
-50                               -45                               -40                               -35

Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro
                               -30                               -25                               -20

Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala
                               -15                               -10                               -5

Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ser
      1                               5                               10

Gly Tyr Val Pro Gly Ser Val Ser Ala Ala Phe Val Thr Cys Pro Arg
15                               20                               25                               30

```

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -24...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.9
 seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

```

Met Pro Ala Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg
      -20                      -15                      -10
Val Leu Leu Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro
      -5                      1                      5
Ala Ser Asp Ser Gly Ser Gly Tyr Val Pro Gly Ser Val Ser Ala Ala
      10                      15                      20
Phe Val Thr Cys Pro Asn Glu Lys Val Ala Lys Glu Ile Ala Arg Ala
      25                      30                      35                      40
Val Val Glu Lys Arg Leu Ala Ala Cys Val Asn Leu Ile Pro Gln Ile
      45                      50                      55
Thr Ser Ile Tyr Glu Trp Lys Gly Xaa Ile Glu Glu Asp Ser Glu Val
      60                      65                      70
Leu Met Met Ile Lys Thr Gln Ala
      75                      80

```

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (D) DEVELOPMENTAL STAGE: Fetal
 (F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -92...-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FLLLTVALLASYS/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

```

Met Glu Ala Ser Trp Gly Ser Phe Asn Ala Glu Arg Gly Trp Tyr Val
      -90                      -85                      -80
Ser Val Gln Gln Pro Glu Glu Ala Glu Ala Glu Glu Leu Ser Pro Leu
      -75                      -70                      -65

```

Leu Ser Asn Glu Leu His Arg Gln Arg Ser Pro Gly Val Ser Phe Gly
 -60 -55 -50 -45
 Leu Ser Val Phe Asn Leu Met Asn Ala Ile Met Gly Ser Gly Ile Leu
 -40 -35 -30
 Gly Leu Ala Tyr Val Met Ala Asn Thr Gly Val Phe Gly Phe Ser Phe
 -25 -20 -15
 Leu Leu Leu Thr Val Ala Leu Leu Ala Ser Tyr Ser Val His Leu Leu
 -10 -5 1
 Leu Ser Met Cys Ile Gln Thr Ala Val Thr Ser Tyr Glu Asp Leu Gly
 5 10 15 20
 Leu Phe Ala Phe Gly Leu Pro Gly Leu
 25

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6
seq FFLLLRFFLRIDG/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp
 -15 -10 -5
 Gly Val Pro
 1

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -19...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FIVGIYFLSSCRA/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser
-15 -10 -5
Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp
1 5 10
Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu
15 20 25

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -23...-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq VLLLAALPPVLLP/GA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Ala Ala
-20 -15 -10
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
-5 1 5
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
10 15 20 25
Tyr Gln Pro Met Pro Leu Xaa Ala Ser Leu Glu Ile Glu
30 35

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq LLSACLVTWGLG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Pro His Ser Ser Leu His Pro Ser Ile Pro Cys Pro Arg Gly His
-35 -30 -25

Gly Ala Gln Lys Ala Ala Leu Val Leu Leu Ser Ala Cys Leu Val Thr
-20 -15 -10

Leu Trp Gly Leu Gly Glu Pro Pro Glu His Thr Leu Arg Tyr Leu Val
-5 1 5 10

Leu Xaa Leu Ala Ser Leu Gln Leu Gly
15 20

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3
seq HLLLLLLPAPTLK/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Gly Ala Trp Gly Arg Gly Trp Pro Trp Glu Glu Arg Gln Gly His
 -25 -20 -15

His Leu Leu Leu Leu Leu Pro Ala Pro Thr Leu Lys Gly Leu Gly
 -10 -5 1

Ala Ala Gln Leu Pro Leu Cys Pro Ser Gly Gly Leu Ser Pro Leu Leu
 5 10 15

Thr Leu Leu Gln Ser Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -75..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq LLFIIGLIGCCAT/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

Met Gly Gln Cys Gly Ile Thr Ser Ser Lys Thr Val Leu Val Phe Leu
 -75 -70 -65 -60

Asn Leu Ile Phe Trp Gly Ala Ala Gly Ile Leu Cys Tyr Val Gly Ala
 -55 -50 -45

Tyr Val Phe Ile Thr Tyr Asp Asp Tyr Asp His Phe Phe Glu Asp Val
 -40 -35 -30

Tyr Thr Leu Ile Pro Ala Val Val Ile Ile Ala Val Arg Ala Leu Leu
 -25 -20 -15

Phe Ile Ile Gly Leu Ile Gly Cys Cys Ala Thr Ile Arg Glu Ser Arg
 -10 -5 1 5

Cys Gly Leu Ala Thr Phe Val Ile Ile Leu Leu Val Phe Val Thr
 10 15 20

Glu Val Val Val Val Val Leu Gly Tyr Val Tyr Arg Ala Lys Val Glu
 25 30 35

Asn Glu Val Asp Arg Ser Ile Gln Lys Val Tyr Lys
 40 45

(2) INFORMATION FOR SEQ ID NO: 528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7
seq IGHFCLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

```

Met Pro Xaa Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65                      -60                      -55                      -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
                      -45                      -40                      -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
                      -30                      -25                      -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
                      -15                      -10                      -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
      1                      5                      10                      15

Ser Xaa Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
                      20                      25                      30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
      35                      40                      45

Val Trp Lys
      50

```

(2) INFORMATION FOR SEQ ID NO: 529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.7
seq LLLSLFFPLRISL/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

```

Met Leu Leu Leu Ser Leu Phe Phe Pro Leu Arg Ile Ser Leu Ser Pro
      -10                      -5                      1
Ser Asn His Leu Trp Ser Ala Ser Ser Gly
      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq LILVLQLLLRIRR/NR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

```

Met Glu Thr Gly Glu Arg Ala Arg Leu Ile Leu Ile Leu Val Leu Gln
      -20                      -15                      -10
Leu Leu Leu Arg Ile Arg Arg Asn Arg Gln Gln Arg Cys Xaa Ala Ser
      -5                      1                      5
Ser Ala Thr Ala Pro Ser Ser His Gly Cys Asp Leu Arg Gly Gly Lys
      10                      15                      20                      25
Leu Asn Phe Lys Thr Thr Pro Met Asp Ala Asp Ser Asp Val Ala Leu
      30                      35                      40
Asp Ile Leu Ile Thr Asn Val Val Cys Val Phe Arg Thr Arg Cys Arg

```

45

50

55

(2) INFORMATION FOR SEQ ID NO: 531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -41..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.4
seq ILGCSSVCQLCTG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Cys Gly Xaa Xaa Phe Ser Leu Pro Cys Leu Arg Leu Phe Leu Val
-40 -35 -30
Val Thr Cys Tyr Xaa Leu Leu Leu Leu His Lys Gln Ile Leu Gly Cys
-25 -20 -15 -10
Ser Ser Val Cys Gln Leu Cys Thr Gly Arg Gln Ile Asn Cys Arg Asn
-5 1 5
Leu Gly Leu Ser Ser Ile Leu Arg Ile Phe Leu Lys Val Gln Phe Phe
10 15 20
Cys Ile
25

(2) INFORMATION FOR SEQ ID NO: 532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -73..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.4
 seq ACCFLSAFSPTLT/KS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

```

Met Asn Pro Val Thr Glu Ser Pro Ser Cys Leu Phe Ser Pro Pro Ser
    -70              -65              -60

Glu Ser Ala Leu Ala Ser Gln Leu Ala Leu Ser Ala Ser Cys Asp Gln
    -55              -50              -45

Arg Ala Pro Phe Ser Leu Ala Gly Val Xaa Ser Xaa Xaa Pro Arg Leu
    -40              -35              -30

Ala Ser Arg Gln Val Ala Pro Pro Phe Gly Ser Arg Ala Cys Cys Phe
    -25              -20              -15              -10

Leu Ser Ala Phe Ser Pro Thr Leu Thr Lys Ser Ala Ala Ala Thr Ser
    -5              1              5

Thr Ala His Thr Phe Leu Ala Asn Gln Leu Ser Cys Leu Phe Thr Lys
    10              15              20

Cys Leu His Asn Asn Tyr Ser Ser Ser Leu Arg Leu Thr Lys Lys Gln
    25              30              35

Glu Lys Ser Thr Thr Pro Gln
    40              45
  
```

(2) INFORMATION FOR SEQ ID NO: 533:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq LGLSVLLTAATVA/GV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

```

Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
    -20              -15              -10

Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
  
```

-5

1

5

(2) INFORMATION FOR SEQ ID NO: 534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq GVGLVTLLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:-534:

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
-25 -20 -15

Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
-10 -5 1 5

Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Ser Glu Lys Tyr Leu
10 15 20

Leu Arg Leu Leu Asp Lys Thr Thr Pro Gly
25 30

(2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE: -

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -51..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq VLLLSMAXLVXXS/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Tyr Pro Ser Tyr Leu Leu Ile Xaa Pro Pro Ile Pro Ser Gln Phe
 -50 -45 -40

Leu Lys Gln Cys Xaa Pro Pro Thr Leu Ser Asp Pro Phe Leu Pro Leu
 -35 -30 -25 -20

Ala Leu Arg Ser Leu Asp Val Leu Leu Leu Ser Ser Ala Xaa Leu Val
 -15 -10 -5

Xaa Xaa Ser Ser Pro Leu Glu Phe Ile Arg
 1 5

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq ILLXTFQTWCLR/IS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Glu Gln Lys His Arg Xaa Glu Leu Glu Gln Leu Lys Leu Xaa Thr
 -30 -25 -20

Lys Glu Asn Lys Ile Leu Leu Leu Xaa Thr Phe Gln Thr Trp Cys Leu
 -15 -10 -5

Arg Ile Ser His Leu Gly Tyr Gln Lys His Xaa Arg Xaa Gly Cys Leu
 1 5 10 15

Asp Xaa Arg Ser Ser Leu Cys Cys Pro Trp
 20 25

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq TLKFLTLQKSNA/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Met Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr
-20 -15 -10
Leu Leu Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His
-5 1 5
Asp Glu Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu
10 15 20 25
Cys Lys Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile
30 35 40
Tyr Pro Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn
45 50 55
Ala Gly Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn
60 65 70
Phe Leu Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr
75 80 85
Ile Phe Glu
90

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27...-1

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.9
 seq ALALAXAPDLAQA/PL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

```

Met Asp Ser Ala Ala Cys Ala Ala Ala Ala Thr Pro Val Pro Ala Leu
  -25          -20          -15
Ala Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro
  -10          -5          1          5
Gly Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn
          10          15          20
Gly Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Thr Leu Ser Ser Thr
          25          30          35
Asn Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly
          40          45          50
Gly Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His
          55          60          65
Pro Val Arg Leu Phe Trp
          70          75
  
```

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ILGLLGGLTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

```

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
          -20          -15          -10
Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
          -5          1          5
Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
  
```

10 15 20
 Gly Leu Trp Met Glu Cys Ala Thr Xaa Ser Thr Gly Ile Thr Gln Cys
 25 30 35 40
 Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala Asp Ile Gln Ala Ala
 45 50 55
 Gln Ala Met Met Val Thr Ser Ser Ala Ile Ser Ser Leu Ala Cys Ile
 60 65 70
 Ile Ser Val Val Gly Met Arg Cys Thr Val Phe Cys Gln Glu Ser Arg
 75 80 85
 Ala Arg
 90

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq ILGLLGLLGLTLVA/ML

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu Leu
 -20 -15 -10
 Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp Lys Thr
 -5 1 5
 Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly Phe Ser Lys
 10 15 20
 Gly Leu Trp Met Glu Cys Ala
 25 30

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LLCECLLLVAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

```

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Val Ala Gly
  -15                      -10                      -5
Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr
   1                      5                      10
Asp Ala Ala Ser Gly Thr Met Arg Lys Ser
  15                      20

```

(2) INFORMATION FOR SEQ ID NO: 542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -22..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.5
seq LWYVCPSPGAWM/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

```

Met Ala Ser Arg Leu Cys Gly Gly Ala Leu Trp Tyr Val Cys Pro Cys
  -20                      -15                      -10
Pro Ser Gly Ala Trp Met Val Pro Gly
  -5                      1

```

(2) INFORMATION FOR SEQ ID NO: 543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LGYLVLSEGAVLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

Met Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu
-25 -20 -15
Gly Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp
-10 -5 1
Leu Glu Asn Asp Glu Gln Ala Xaa Ser Ala Ile Ser Glu Leu Val Ser
5 10 15 20
Thr Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Arg
25 30 35

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -42..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq ITGVILAVGNG/KV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

```

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
  -40                      -35                      -30

Phe Lys Ser Val Leu Leu Ile Xaa Thr Xaa Ile Xaa Trp Ile Thr Gly
  -25                      -20                      -15

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
  -10                      -5                      1                      5

Tyr Phe Xaa Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Xaa Leu
      10                      15                      20

Ile Ala Thr Gly Thr Val Xaa Ile Leu Leu Gly Tyr Arg
      25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq VLLGSGLTILSQP/LM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

```

Met Ala Asp Ala Ala Ser Gln Val Leu Leu Gly Ser Gly Leu Thr Ile
-20                      -15                      -10                      -5

Leu Ser Gln Pro Leu Met Tyr Val Lys Val Leu Ile Gln Val Gly Tyr
      1                      5                      10

Glu Pro Leu Pro Pro Thr Ile Gly Arg Asn Ile Phe Gly Arg Gln Val
      15                      20                      25

Xaa Xaa Leu Pro Xaa Leu Phe Ser Tyr Ala Gln His Gly
      30                      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids

(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -20..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq ALIFGGFISLIGA/AF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
-20 -15 -10 -5

Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro His Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq LWCFHLVVLSLYS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Pro His Gly Leu Trp Cys Phe His Leu Val Val Leu Ser Leu Tyr
-15 -10 -5

Ser Ser Val Ala Thr Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq SLVAVFLSCGLIS/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

```

Met Ser Leu Val Ala Val Phe Leu Ser Cys Gly Leu Ile Ser Lys Asn
      -10                      -5
His Met Leu Leu Asn Leu Pro Gly Ile Leu Ile Pro His Asn Ala Asn
      5                      10                      15
His Leu Leu
      20

```

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5
seq GALAVSAVPVLS/AM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

```

Met Met Lys Arg Ala Ala Ala Ala Val Gly Gly Ala Leu Ala Val
      -20                      -15                      -10
Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe Thr Gly Ala Gly
      -5                      1                      5

```

Ile Ala Ala Ser Ser Ile Ala Ala His Gly
 10 15

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
 seq LISFSWFANYIRA/GT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp Met Lys Lys Val
 -30 -75 -70

Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser Gln Tyr Trp Tyr
 -65 -60 -55 -50

Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu Phe Ser Ile Ala
 -45 -40 -35

Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile Ile His His Val
 -30 -25 -20

Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala Asn Tyr Ile Arg
 -15 -10 -5

Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser Asp Tyr Leu Leu
 1 5 10 15

Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys Asn Thr Cys Asn
 20 25 30

Asn Ile Phe Thr Val Phe Ala Ile Val Phe Ile Ile Thr Arg Leu Val
 35 40 45

Ile Leu Pro Phe Trp Ile Leu His Cys
 50 55

(2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.8
seq SLFIYIFLTCSNT/SP.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Met Ile Ile Ser Leu Phe Ile Tyr Ile Phe Leu Thr Cys Ser Asn Thr
-15 -10 -5
Ser Pro Ser Tyr Gln Gly Thr Gln Leu Gly Leu Gly Leu Pro Ser Ala
1 5 10 15
Gln Trp Trp Pro Leu Thr Gly Arg Arg Met Gln Cys Cys Arg Leu Phe
20 25 30
Cys Phe Leu Leu Gln Asn Cys Leu Phe Pro Phe Pro Leu His Leu Ile
35 40 45
Gln His Asp Pro Cys Glu Leu Val Leu Thr Ile Ser Gly Thr
50 55 60

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LQMLLG FVGRSKS/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

```

Met Ala Ala Glu Leu Val Glu Ala Lys Asn Met Val Met Ser Phe Arg
-30                -25                -20

Val Ser Asp Leu Gln Met Leu Leu Gly Phe Val Gly Arg Ser Lys Ser
-15                -10                -5

Gly Leu Lys His Glu Leu Val Thr Arg Ala Leu Gln Leu Val Gln Phe
1                5                10                15

Asp Cys Ser Pro Glu Leu Phe Lys Lys Ile Lys Glu Leu Tyr Glu Thr
20                25                30

Arg Tyr Ala Lys Lys Asn Ser Glu Pro Ala Pro Gln Pro His Arg Pro
35                40                45

Leu Asp Pro Leu Thr Gly
50

```

(2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -60..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq VHALCPLSPLVTT/GC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

```

Met Thr Gly Leu Ser Met Xaa Gly Gly Gly Ser Xaa Xaa Gly Asp Val
-60                -55                -50                -45

Xaa Pro Xaa Tyr Tyr Gly Lys Xaa Gly Pro Leu Arg Xaa Leu Pro Glu
-40                -35                -30

Pro Ser Gly Pro Leu Pro Pro Ser Ser Gly Leu Ser Gln Pro Gln Val
-25                -20                -15

His Ala Leu Cys Pro Leu Ser Pro Leu Val Thr Thr Gly Cys Cys Gly
-10                -5                1

Gln Ala Ala
3

```

(2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq GLLGXGLXXXSLT/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Xaa Glu Trp Leu Thr Ile
-30 -25 -20

Gln Gly Gly Leu Leu Gly Xaa Gly Leu Xaa Xaa Xaa Ser Leu Thr Ala
-15 -10 -5 1

Gly

(2) INFORMATION FOR SEQ ID NO: 555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -54..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSFSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu

```

-50              -45              -40
Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro
-35              -30              -25
Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val
-20              -15              -10
Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
-5              1              5              10
Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys
15              20              25
Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
30              35              40
Gly Leu Gly Thr Ala Tyr Ile Xaa Xaa Met Lys His Ala Gln Glu Thr
45              50              55
Thr Ser Leu Leu Trp Xaa Leu Ile Ser His
60              65

```

(2) INFORMATION FOR SEQ ID NO: 556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LLDSSLMASGTAS/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

```

Met Asp Lys Asp Ser Gln Gly Leu Leu Asp Ser Thr Leu Met Ala Ser
-20              -15              -10              -5
Gly Thr Ala Ser Arg Ser Glu Asp Glu Glu Ser Leu Ala Gly Gln Lys
1              5              10
Arg Ala Ser Ser Gln Ala Leu Gly Thr Gly
15              20

```

(2) INFORMATION FOR SEQ ID NO: 557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CLAVSWEAAGCHG/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

Met Gly Leu Leu Thr Phe Gly Tyr Ile Glu Xaa Xaa Xaa Lys Thr Glu
-35 -30 -25
His Asn Pro Asp His His Ser Cys Leu Ala Val Ser Trp Glu Ala Ala
-20 -15 -10 -5
Gly Cys His Gly Ala Gly Thr Gln Gln Ser Pro Leu Gly Val Ala Gly
1 5 10
Pro Trp Arg Pro Arg Pro Pro Cys Val Gly Ser Leu Leu Ala Ala Arg
15 20 25
Ser Leu His Lys Gln Val Ile Leu Phe Gly Leu Leu Gly Phe Ala Tyr
30 35 40
Asp His Trp
45

(2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq YAAVAJVLAVGES/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Met Gly Leu Tyr Ala Ala Val Ala Gly Val Leu Ala Gly Val Glu Ser
 -15 -10 -5

Arg Gln Gly Ser Asn Gln Gly Ala Gly Val Leu Gln Gln Leu Pro Glu
 1 5 10 15

Arg Glu Xaa Ala Val Arg Ala Gly Val Arg Xaa Ala Ala Leu Leu Arg
 20 25 30

Arg Ala Gly Xaa Arg Asp Leu Gln Arg Arg Pro Pro Gln Cys Glu Glu
 35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO: 559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -62..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LDAVIASAGLLRA/EK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
 -60 -55 -50

Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
 -45 -40 -35

Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
 -30 -25 -20 -15

Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
 -10 -5 1

Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 5 10 15

Gly Lys Gly Phe Arg Gly Gly Gly Arg Trp Lys Ala Arg
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq WLLRLAYLADIFT/KL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

```

Met Gly Ala Gln His Thr Ala Leu Leu Leu Asn Thr Glu Val Arg Trp
      -60                      -55                      -50

Leu Ser Arg Gly Lys Val Leu Val Arg Leu Phe Glu Leu Arg Arg Glu
      -45                      -40                      -35

Leu Leu Val Phe Met Asp Ser Ala Phe Arg Leu Ser Asp Cys Leu Thr
      -30                      -25                      -20

Asn Ser Ser Trp Leu Leu Arg Leu Ala Tyr Leu Ala Asp Ile Phe Thr
      -15                      -10                      -5

Lys Leu Asn Glu Val Asn Leu Ser Met Gln Gly Lys Asn Val Thr Val
      1                      5                      10                      15

Phe Thr Val Phe Asp Lys Met Ser Ser Leu Leu Arg Lys Leu Glu Phe
      20                      25                      30

Trp Ala Ser Ser Val Glu Glu Glu Asn Phe Asp Cys Phe Pro Thr Leu
      35                      40                      45

Ser Asp Phe Leu Thr Glu Ile Asn Ser Thr Val Asp Lys Asp Ile Cys
      50                      55                      60

Ser Ala Ile Val Gln His Leu Arg Gly Leu Arg Ala Thr Leu Leu Lys
      65                      70                      75                      80

Tyr Phe Pro Val Thr Asn Asp
      85

```

(2) INFORMATION FOR SEQ ID NO: 561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -25..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq LVVMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

```

Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Val Met
-25                -20                -15                -10

Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
          -5                1                5

Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asn Met
      10                15

```

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Heart

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -51..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.9
 seq GKLLQLVLGCAIS/CE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

```

Met Val Leu Arg Ser Leu Val Glu Tyr Ser Gln Asp Val Leu Ala His
-50                -45                -40

Pro Val Ser Glu Glu His Leu Pro Asp Val Ser Leu Ile Gly Glu Phe
-35                -30                -25                -20

Ser Asp Pro Ala Glu Leu Gly Lys Leu Leu Gln Leu Val Leu Gly Cys

```

Ala Ile Ser Cys Glu Lys Lys Gln Asp His Ile Gln Arg Ile Met Thr
1 5 10
Leu Glu Glu Ser Val Gln His Val Val Met Glu Ala Ile Gln Glu Leu
15 20 25
Met Thr Lys Asp Thr Pro Asp Ser Leu Ser Pro Glu Thr Tyr Gly Asn
30 35 40 45
Phe Asp Ser Gln Ser Arg Ser Thr Gly
50

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -13..-1
- (C) IDENTIFICATION METHOD: Von Helme matrix
- (D) OTHER INFORMATION: score 3.9
seq MIHGFCLAPTSA/KN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Ile His Gly Phe Cys Leu Ala Pro Thr Thr Ser Ala Lys Asn Ala
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: -17..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: . score 3.7
 seq RTWCLACVEASPG/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Xaa Cys Pro Arg Thr Trp Cys Leu Ala Cys Val Glu Ala Ser Pro
 -15 -10 -5
 Gly Gln Pro Phe Leu Pro Pro Arg Pro Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -21..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq ETCALASHSGSSG/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Asp Val Glu Asp Gly Glu Glu Thr Cys Ala Leu Ala Ser His
 -20 -15 -10
 Ser Gly Ser Ser Gly Ser Lys Ser Gly Gly Asp Lys Met Phe Ser Leu
 -5 1 5 10
 Lys Lys Trp Asn Ala Val Ala Met Trp Ser Trp Asp Val Glu Cys Asp
 15 20 25
 Thr Cys Ala Ile Cys Arg Val Gln Val Met Asp Ala Cys Xaa Arg Cys
 30 35 40
 Gln Ala Gly
 45

(2) INFORMATION FOR SEQ ID NO: 566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids
 (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN .

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -26..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq IIMFLLIIVCGSP/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

Met Phe Lys Val Ala Ala Pro Pro Met Leu Ile Xaa Xaa Ile Ile Met
-25 -20 -15

Phe Leu Leu Ile Ile Val Cys Gly Ser Pro Arg Pro
-10 -5 1

(2) INFORMATION FOR SEQ ID NO: 567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -21..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq FXMCLWSLRNLFS/RC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

Met Asp Phe Trp Asp Pro Ala Val Phe Xaa Met Cys Leu Trp Ser Leu
-20 -15 -10

Arg Asn Leu Phe Ser Arg Cys Ser Pro Cys Leu Thr Glu Ile Ser Leu
-5 1 5 10

His Leu Val His Leu Thr Ala Glu Lys Lys Gln His Gly Ser Asn Asn
15 20 25

Gly Ser Ala
30

(2) INFORMATION FOR SEQ ID NO: 568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -34..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq SVPLLSLSHSIGI/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Ser Pro Ala Gly Lys His Asn Ser Glu Ser Lys Phe Thr Phe Phe
 -30 -25 -20

Val Ala Leu Asp Gly Ser Val Pro Leu Leu Ser Leu Ser His Ser Ile
 -15 -10 -5

Gly Ile Ser Pro Thr Arg
 1

(2) INFORMATION FOR SEQ ID NO: 569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LVCVGLHTEGPWG/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met His Trp Ala Leu Val Cys Val Gly Leu His Thr Glu Gly Pro Trp
 -15 -10 -5

Gly Arg Pro Ser Gly Leu Ala Ser Ala Ser Gly Met Asp Arg Ala Arg
 1 5 10 15

Gln Ala Ser Glu Leu Pro Pro Pro Gly Ala Ser Gln Thr Pro Gln
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney.

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -72..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Phe Gly Ala Ala Ala Arg Ser Ala Asp Leu Val Leu Leu Glu Lys
 -70 -65 -60

Asn Leu Gln Ala Ala His Gly Tyr Ala Gln Glu Asp Arg Glu Arg Met
 -55 -50 -45

His Arg Xaa Ile Val Ser Leu Xaa Gln Asn Leu Leu Asn Phe Met Ile
 -40 -35 -30 -25

Gly Ser Ile Leu Asp Leu Trp Gln Cys Phe Leu Trp Phe Tyr Ile Gly
 -20 -15 -10

Ser Ser Leu Asn Gly Thr Arg Gly Lys Arg Val Pro Ala His Phe
 -5 1 5

(2) INFORMATION FOR SEQ ID NO: 571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -27..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq VVALLIVCDVPSA/SA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
-25 -20 -15

Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Arg
-10 -5

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LLLQPSMIQEVWT/XY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

Met Val Val Leu Leu Leu Gln Pro Ser Met Ile Gln Glu Val Trp Thr
-15 -10 -5

Xaa Tyr Ala Asn Leu Phe His Ser Phe Phe Val Asp Asn Pro Phe Gln
1 5 10 15

Lys Glu Cys Phe His Gln Lys Asn Trp Tyr His Ile Thr Leu Met Gln
20 25 30

Arg Thr Val Gly Thr Trp Arg Ile Leu Pro Asn Phe Leu Lys His Asp
35 40 45

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -31..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq LAVLLSLAPSASS/DI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

Met Leu His Leu His Xaa Ser Cys Leu Cys Phe Arg Ser Trp Leu Pro
-30 -25 -20

Ala Met Leu Ala Val Leu Leu Ser Leu Ala Pro Ser Ala Ser Ser Asp
-15 -10 -5 1

Ile Ser Ala Ser Arg Pro Asn Ile Leu Leu Leu Met Ala Asp Asp Leu
5 10 15

Gly Ile Gly Asp Ile Gly Cys Tyr Gly Asn Asn Thr Met Arg Thr Pro
20 25 30

Xaa Ile Asp Arg Leu Ala Glu Asp Gly Val Lys Leu Thr Gln His Ile
35 40 45

Ser Ala Ala Ser Leu Cys
50 55



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

| | | |
|---|-----------|--|
| (51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47 | A3 | (11) International Publication Number: WO 99/06554 (43) International Publication Date: 11 February 1999 (11.02.99) |
| (21) International Application Number: PCT/IB98/01238 (22) International Filing Date: 31 July 1998 (31.07.98) (30) Priority Data: 08/905,134 1 August 1997 (01.08.97) US (71) Applicant (for all designated States except US): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR). (72) Inventors; and (75) Inventors/Applicants (for US only): DUMAS MILNE ED- WARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire de Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). LACROIX, Bruno [FR/FR]; 93, route de Vourles, F-69230 Saint-Genis Laval (FR). (74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR). | | (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> (88) Date of publication of the international search report: 27 May 1999 (27.05.99) |
| (54) Title: 5' ESTs FOR SECRETED PROTEINS EXPRESSED IN MUSCLE AND OTHER MESODERMAL TISSUES (57) Abstract <p>The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be obtained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.</p> | | |

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INTERNATIONAL SEARCH REPORT

In tional Application No

PCT/IB 98/01238

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-------------------------|
| E | <p>WO 98 44114 A (INCYTE PHARMACEUTICALS INC. (US); HILLMAN JENNIFER L.; GOLI SURYA K.) 8 October 1998 see abstract see page 12, line 5-14 see page 42 - page 43 see page 46 - page 47; claims --- -/-</p> | <p>1-11, 15-37</p> |

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

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Date of the actual completion of the international search

10 November 1998

Date of mailing of the international search report

01 03 99

Name and mailing address of the ISA

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Macchia, G

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 98/01238

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------|
| E | WO 98 42738 A (HUMAN GENOME SCIENCES INC. (US); YOUNG PAUL ET AL.) 1 October 1998 see page 40, line 34 - page 41, line 35 Gene No.46 see page 79 see page 100, line 23-25 Seq.ID:56 see page 209 - page 210 Seq.ID:110 see page 259 - page 260 Seq.ID:170 see page 297 - page 298 Seq.ID:224 see page 331 - page 332 see page 381 - page 384; claims --- | 1-28, 34-37 |
| X | Database EMBL Emest7, Entry HS1150166 Accession number AA232452 6 March 1997 96% identity with Seq.ID:38 nt.41-140 XP002083765 | 1-11, 15-37 |
| Y | see the whole document --- | 12-14 |
| Y | YOKOYAMA-KOBAYASHI M. ET AL.: "A signal sequence detection system using secreted protease activity as an indicator" GENE, vol. 163, 1995, pages 193-196, XP002053953 see abstract --- | 12,13 |
| Y | LIN Y. ET AL.: "Inhibition of nuclear translocation of transcription factor NF-kB by a synthetic peptide containing a cell membrane-permeable motif and nuclear localization sequence" JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 24, 16 June 1995, pages 14255-14258, XP002050723 cited in the application see abstract --- | 14 |
| A | OZAWA M.: "Cloning of a human homologue of mouse reticulocalbin reveals conservation of structural domains in the novel endoplasmic reticulum resident Ca ²⁺ -binding protein with multiple EF-hand motifs" JOURNAL OF BIOCHEMISTRY, vol. 117, 1995, pages 1113-1119, XP002070128 --- -/-- | |

INTERNATIONAL SEARCH REPORT

Int. l. Application No

PCT/IB 98/01238

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| A | SCHÄFER B.W. AND HEIZMANN C.W.: "The S100 family of EF-hand calcium-binding proteins: functions and pathology" TIBS TRENDS IN BIOCHEMICAL SCIENCES, vol. 21, no. 4, April 1996, page 134-140 XP004050923 --- | |
| A | WO 96 34981 A (GENSET (FR); MERENKOVA IRENA NICOLAEVNA; DUMAS MILNE EDWARDS JEAN) 7 November 1996 cited in the application --- | |
| A | KATO S. ET AL.: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1994, pages 243-250, XP002081364 cited in the application --- | |
| A | EP 0 625 572 A (KANAGAWA ACAD OF SCIENCE AND TECHNOL FOUNDATION (JP); KATO S; SEKINE S) 23 November 1994 cited in the application --- | |
| A | CARNINCI P. ET AL.: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996, pages 327-336, XP002081729 cited in the application --- | |
| A | WO 97 07198 A (GENETICS INSTITUTE INC (US); JACOBS K; MCCOY JM; KELLEHER K; CARLIN M) 27 February 1997 --- | |
| A | TASHIRO K. ET AL.: "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 30 July 1993, pages 600-603, XP000673204 --- | |
| A | HEIJNE VON G.: "A new method for predicting signal sequence cleavage sites" NUCLEIC ACIDS RESEARCH, vol. 14, no. 11, 1986, pages 4683-4690, XP002053954 cited in the application ----- | |

INTERNATIONAL SEARCH REPORT

International application No.

PCT/IB 98/01238

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

See extra sheet, Invention 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: Claims 1-37 all partially

Nucleic acid comprising the sequence as in Seq.ID:38, complementary sequence, fragments, hybridizing sequences. Polypeptide comprising a signal peptide encoded by said nucleotide sequence. Vector encoding a fusion protein comprising said signal peptide. A method of directing the extracellular secretion of a polypeptide by means of said vector. Method of importing a polypeptide into a cell by means of said signal peptide. A method for making a cDNA encoding a secretory protein, partially encoded by said nucleotide sequence, corresponding cDNA. Polypeptide encoded by said nucleotide sequence, comprising a sequence as in Seq.ID:306, method of making said polypeptide. Method of obtaining a promoter located upstream of said nucleotide sequence, promoter thereof.

Inventions 2-268: Claims 1-37 all partially

Idem as subject 1 but limited to each of the DNA sequences as in Seq.ID:39-305, and corresponding polypeptides, where invention 2 is limited to Seq.ID:39 and 307, invention 3 is limited to Seq.ID:40 and 308,....., invention 147 is limited to Seq.ID:305 and 573).

For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/IB 98/01238

| Patent document cited in search report | Publication date | Patent family member(s) | Publication date |
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| WO 9844114 A | 08-10-1998 | AU 6787598 A | 22-10-1998 |
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| | | AU 6768596 A | 12-03-1997 |
| | | CA 2227220 A | 06-02-1997 |
| | | CA 2229208 A | 27-02-1997 |
| | | EP 0839196 A | 06-05-1998 |
| | | EP 0851875 A | 08-07-1998 |
| | | WO 9704097 A | 06-02-1997 |